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(without alignments)
1378.235 Million cell updates/sec
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3347
1 MSERKEGRGKGKKKKERGS......QEEIQARLSSVIANQDPIAV 645
                                                                                                                     April 12, 2005, 14:21:26; Search time 181 Seconds
                                                                                                                                                                                                                                                                                                                                                                                          2105692
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                               OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1: geneseqp1980s:*
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3: geneseqp2000s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query Match	Length	DB	ID	Description	
-	3347	100.0	645	~	AAY06635	Aay06635 Herugelin	i i
7	3347	100.0	645	m	AAB36793	Human	her
٣	3347	100.0	645	1	ADB67619	Human	her
4	3347	100.0		æ	ADN48871	Human	her
ហ	3347	100.0	67	7	AAR29571	Human	her
ø	3347	100.0	67	m	AAY71172	2 Human	Her
7	3347	100.0		4	AAU09887	Human	her
œ	3344	99.9		٣	AAY71198	Human	Her
0	3344	99.9	675	m	AAY71188	Human	Her
10	3344	99.9	675	ო	AAY71189	Human	Her
11	3344	99.9	675	m	AAY71191	Human	Her
12	3343	99.9	675	m	AAY71182	Human	Her
13	3343	6.66	675	m	AAY71203	Human	ler
14	3343	99.9	675	m	AAY71194	Human	ler
15	3342	99.9	675	m	AAY71180	Human	ler
16	3342	99.9	675	m	AAY71185	Human	Her
17	3342	99.9	675	m	AAY71197	Human	ler
18	3341	99.8	675	m	AAY71186 .		ler
19	3341	99.8	675	m	AAY71183	Human	Her
20	3341	99.8	675	ო	AAY71190	Aay71190 Human H	Her
21	3341	99.8	675	m	AAY71181	Human	Her
22	3341	99.8	675	m	AAY71187	Human	Her
23	3341	99.8	675	m	AAY71201	Aay71201 Human H	Her
24	3341	99.8	675	ო	AAY71184	Human	Her
25	3340	99.8	675	m	AAY71192	Aav71192 Human H	Her

	Aw74489 Amino aci Aaw74491 Amino aci Aaw74487 Amino aci Aaw74496 Amino aci
AAY71202 AAY71200 AAY71195 AAY71178 AAX711196 AAW74994 AAY71199 AAW711199 AAG67949 AAW74493 AAW74509 AAW74688	AAW74489 AAW74491 AAW74487 AAW7496
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## ALIGNMENTS

Heregulin-beta-1; HRG-alpha; human; ligand; HER2; HER3; HER4; receptor; lung surfactant; respiratory distress syndrome; emphysema; AAY06635 standard; protein; 645 AA. lung surfactant; respiratory distr epithelial growth factor; therapy. 99WO-US002390 98US-00020598. (GETH ) GENENTECH INC. (IOWA ) UNIV IOWA RES FOUND. (first entry) Sliwkowski M, Kern JA; WPI; 1999-494213/41. Herugelin-beta-1. N-PSDB; AAX87701. Homo sapiens. 26-OCT-1999 W09939729-A2 03-FEB-1999; 04-FEB-1998; 12-AUG-1999. AAY06635; 

Heregulin ligands can be used to induce epithelial cell growth, and to promote repair and healing of tissue damage or injury.

Disclosure; Page 87-90; 120pp; English.

This sequence represents heregulin-beta-1 (HRG-beta-1) deduced from HRG-beta-1 cDNA (see AAX8701). The invention provides HRG ligands, including HRG-beta-1, that have affinity for and stimulate HRR2, HER3 and/or HER4 receptors in autophosphorylation. A new method of treating respiratory distress syndrome in humans uses HRR2, HER3 and/or HER4 receptor ligands as epithelial growth factors. A novel method of inducing epithelial growth and/or proliferation comprises contacting a normal epithelial cell which expresses HER2, HER3 and/or HER4 receptors with an isolated ligand which extrates HER2, HER3, HER4 receptors or their combination. Also claimed are methods of increasing lung surfactant protein A, or of treating chronic obstructive pulmonary disease, respiratory distress or

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The present invention relates to variants of heregulin that can bind to an BrbB receptor and include a portion of the 175-230 region of native human heregulin-betal. The variants may be used to promote ex vivo survival, proliferation and differentiation of cells, particularly when intended for transplantation. They may also be used to treat a wide range of cancers and diseases of the nervous system, musculature and epithelium
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                                                                                                                                                                                                      Wells JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 3347; DB 3;
llarity 100.0%; Pred. No. 2.2e-204;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                  Ballinger MD,
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98US-00020880
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                                                                                   181 KCABKBKTFCVNGGECFMVKDLSNPSRYLCKCPNBFTGDRCQNYVMASFYKHLGIBFMBA
                                                                                                                            EELYQKRVLTITGICIALLVVGIMCVVAYCKTKKQRKKLHDRLRQSLRSERNNMMNIANG
                                                                                                                                                           241 EELYQXRVLTITGICIALLVVGIMCVVAYCKTKKQRKKLHDRLRQSLRSERNNMMIANG
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                                                                                                                                                                                             PHHPNPPPENVOLVNOYVSKNVISSEHIVEREAETSFSTSHYTSTAHHSTTVTOTPSHSW
DSASANITIVESNEIITGMPASTEGAYVSSESPIRISVSTEGANTSSSTSTSTTGTSHLV
                  KCAEKEKTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCQNYVMASFYKHLGIEFMEA
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(GEOU ) UNIV GEORGETOWN MEDICAL CENT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a non-naturally occurring human epidermal growth factor receptor (HER)-3 variant polypeptide comprising amino acids 19-329 or 20-329 of the 1342 amino acid HER3 polypeptide (ADB67617) or a sequence which differs from native HER3 polypeptide and having amino acid substitutions at residues B43, N44, K51, E64, V66 and V110 of S1, is new. The variant HER-3 specifically binds to the haregulin polypeptide (ADB67619), exhibits an impaired ability to inhibit the interaction between wild-type HER3 and heregulin. The polypeptide is useful for identifying a compound which specifically binds to heregulin binding domain in a HER3 variant polypeptide. The method further involves determining whether the test compound inhibits or enhances the heregulin induced tyrosine kinase activity associated with a HER3 polypeptide. The polypeptide is also useful for determining whether a test compound modulates the interaction between a heregulin polypeptide, and the variant HER-3 polypeptide. The HER-3 polypeptide is also useful for inhibiting the interaction between a heregulin polypeptide and HER3 polypeptide. Set for treating cancer. The polypeptide is also useful for stimulating or activating HER3 receptor. This sequence represents the stimulating or activating HER3 receptor. This sequence represents the vill type human heregulin polypeptide.
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                                                                                                                                                                       cytostatic; human epidermal growth factor receptor-3; HER-3; heregulin; HER2; tyrosine kinase activity; cancer.
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Best Local Similarity 100.0%; Pred. No. 2.2e-204;
Matches 645; Conservative 0; Mismatches 0;
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                                          ADB67619 standard; protein; 645 AA.
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                                                                                                           (first entry)
                                                                                                                                          Human heregulin protein.
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for preparing a composition for diagnosing and treating cancer. The invention is also useful in gene therapy. The present sequence is human heregulin protein.
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                                                                                                                                    1 MSERKEGRGKGKGKKKERGSGKKPESAAGSQSPALPPQLKEMKSQESAAGSKLVLRCETS
                                                                                                                                                            DSASANITIVESNEIITGMPASTEGAYVSSESPIRISVSTEGANTSSSTSTSTTGTSHLV
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Clone lambda heril.idbl (heregulin-beta-1) was identified in a lambda gt10 oligo-dT primed cDNA library derived from human breast carcinoma MDA-MB-231 cells. Labelled synthetic DNA probes corresponding to the 5' and 3' ends of lambda heri6 (see AAQ31541) were used in the hybridisation reaction under high stringency conditions. The HRG-beta-1 clone extends 189 bp longer than lambda heri6 in the 3' direction and supplies a stop codon after val 675. At nucleotide position 205 of lambda heri1.idbl there is an A substituted for G which results in substitution of Gln in place of Arg at position 68 in HRG-beta-1. The other differences occur in the EGF motif of the two HRG proteins. See also AAQ31543-Q31948. (Updated on 25-MAR-2003 to correct PA field.)
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                                                                                                                                               mature HRG-
                                18
/note= "deduced from ORF but initiating MET is at position 31 and the processed N-terminal residue
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                                                                                                              /note= "serine-glycine dipeptide potential glycosaminoglycan addition site - not part alpha sequence"
                                                                                                                                                                                                                             /note= "serine-glycine dipeptide potential glycosaminoglycan addition site"
                                                                                                                                                                                                                                                                                   137. .138
/note= "serine-glycine dipeptide potential
glycosaminoglycan addition site"
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                                                                                                                                                                                                                                                                                                                                                                                                              156. .158 "note= "N-linked glycosylation site" (95. .207
                                                                                                                                                                                                                                                                                                                                                                          150. .152
/note= "N-linked glycosylation site"
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/note= "N-linked glycosylation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  212. .251
/label= EGF motif
/note= "contains 6 cysteines"
278. .300
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'note= "probable"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 6; Fig 8; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91US-00705256.
91US-00765212.
91US-00790801.
92US-00847743.
92US-00880917.
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                                                           Ser32
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                                                 SEYSSLRFKWFKNGNELNRKNKPQNIKIQKKPGKSELRINKASLADSGEYMCKVISKLGN
                                                                                          SEYSSLRFKWFKNGNELMRKNKPQNIKIQKKPGKSELRINKASLADSGEYMCKVISKLGN
                                                                                                                    DSASANITIVESNEIITGMPASTEGAYVSSESPIRISVSTEGANTSSSTSTSTTGTSHLV
                                                                                                                                 211 KCAEKEKTFCVNGGECFWVKDLSNPSRYLCKCPNEFTGDRCQNYVMASFYKHLGIEFMBA
                                                                                                                                                                                                     EELYQKRVLTITGICIALLVVGIMCVVAYCKTKKQRKKLHDRLRQSLRSERNNMMNIANG
                                                                                                                                                                                                                  BELYQKRVLTITGICIALLVVGIMCVVAYCKTKKQRKKTHDRLRQSLRSERNNMMNIANG
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                                      1 MSERKEGRGKGKGKKKERGSGKKPESAAGSOSPALPPOLKEMKSOESAAGSKLVLRCETS
                                                                                                                                                            KCAEKEKTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCQNYVMASFYKHLGIEFMEA
                                                                                                                                                                                                                                           PHHPNPPPENVQLVNQXVSKNVISSEHIVEREAETSFSTSHYTSTAHHSTTVTQTPSHSW
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                   Gaps
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    /note= "Cleavage results in amino terminal fragment

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                  Indels
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         Pred. No. 2.3e-204;
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/label= Initiator_methionine
212. .251
                  Mismatches
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100.08;
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       Local Similarity 100.
nes 645; Conservative
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The patent discloses a method for inducing hair cell generation, or inner ear-supporting cell growth, regeneration, and/or proliferation, by heregulins (HRG), the ligand for HER2-10 enceptors. Heregulin proteins function as activators of HER-2 oncogene and result from alternate splicing of a single gene mapped to chromosome 8p. The two major types, alpha and beta HRG's are based on two variant EGF-like (epidermal growth factor) domains, that differ in their C-terminal ends. This method can be used to increase the number of inner-ear-supporting cells and for treatment of hair cell related hearing disorders and sissase states associated with tissue damage, e.g. ototoxic injury, acoustic assault, degenerative hearing loss, balance impairments, damage associated with surgery or physical injury and inner ear disorders and elated to hair cell dysfunction. The present sequence is the human heregulin, HRG-betal protein, derived from a genomic library. This sequence can be used to construct several variants
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by
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                                                                   91 SEYSSLRFKWFKNGNELNRKNKPQNIKIQKKPGKSELRINKASLADSGEYMCKVISKLGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 SEYSSLRFKWFKNGNELNRKNKPQNIKIQKKPGKSELRINKASLADSGEYMCKVISKLGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for inducing hair cell generation and inner-ear-supporting eregeneration and proliferation, useful for treating hearing
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/label= Growth factor domain
/note= "HRG-beta-GFD"
255. .256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 2; 141pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC
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                                                  Cleavage-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Method for
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disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neonatal pulmonary disease, neonatal respiratory distress syndrome; meconium aspiration syndrome; congenital diaphragmatic hernia; lesion; acute lung injury; cystic fibrosis; surgical wound; resection; growth factor; smoke inhalation; HRG-betal.
                                               PH+PNPPPENVQLVNQYVSKNVISSEHIVEREAETSFSTSHYTSTAHHSTTVTQTPSHSW
                                                                                                                                            RDSPHSERYVSAWTTPARMSPVDFHTPSSPKSPPSEMSPPVSSWTVSMPSMAVSPFMEEE
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                                                                                                                                                                                                                         EPVKKLANSRRAKRTKPNGHIANRLEVDSNTSSQSSNSESETEDERVGEDTPFLGIQNPL
                             PHHPNPPPENVQLVNQYVSKNVISSEHIVEREAETSFSTSHYTSTAHHSTTVTQTPSHSW
                                                                                     SNGHTESILSESHSVIVMSSVENSRHSSPTGGPRGRLNGTGGPRECNSFLRHARETPDSY
                                                                                                      SNGHTESILSESHSVIVMSSVENSRHSSPTGGPRGRLNGTGGPRECNSFLRHARETPDSY
                                                                                                                                                                                                       RPLLLVTPPRLREKKFDHHPQQFSSFHHNPAHDSNSLPASPLRIVEDEEYETTQEYEPAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inducing epithelial cell growth and/or proliferation, useful in the treatment of respiratory disease, comprises use of heregulin ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to inducing epithelial cell growth and/or proliferation comprising contacting a normal epithelial cell, which
                                                                                                                                                                                                                                                                                                                             645
                                                                                                                                                                                                                                                                                                                                            AASLEATPAFRLADSRTNPAGRFSTQEEIQARLSSVIANQDPIAV 675
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N-PSDB; AAS18522.
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02-FEB-1999;
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cc expresses HER2, HER3 and/or HER4 (preferably HER2/HER3, HER2/HER4,
HER3 or HER4) receptors with an isolated ligand such as
heregulin (HR6) which activates HER2, HER3 and/or HER4 receptors. The
method is used for inducing epithalial call (preferably lung cell) growth
and/or proliferation, for increasing lung surfactant protein A and for
treating respiratory disease or emphysema, for treating chronic
cobstructive pulmonary diseases including neonatal respiratory distress
cc obstructive pulmonary diseases including neonatal respiratory distress
cc syndrome, meconium aspiration syndrome, chronic lung disease of the
neonate, congenital diaphragmatic hernia and acute lung injuries
cncluding smoke or chemical inhalation, pneumonitis due to aspiration,
cradiation, near drowning, cystic fibrosis and other epithelial cell
crauma diseases including injuries associated with surgical wounds and
cresections, ulcers, lesions and tissue tears as normal epithelial cell
growth factors. For traating infants/neonates with respiratory distress
as well as youth and adult with poor lung function due to lung injury or
damage. The HRG binds with varying and very high affinity to the HER2,
HER3 and/or HER4 receptors. The method stimulates growth and
cc proliferation of the epithelial cells, repairing and re-establishing the
ccellular barriers of organs and allowing the affected tissue to infection while
ccellular barriers of organs and allowing the affected tissue to develop
normal physiological functions more quickly. Hence the method improves
cc oxygenation and speeds of the development of a barrier to infection while
creating lung cells that are damaged by inhalation of smoke resulting in
creating lung cells that are damaged by inhalation of smoke resulting in
creating lung cells that are damaged by endower of human heregulin
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Best Local Similarity 100.
Matches 645; Conservative
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ear-supporting cell growth, regeneration, and/or proliferation, by
heregulins (HRG), the ligand for HRR2/HRR3 dimeric receptors. Heregulin
proteins function as activators of HER-2 oncogene and result from
alternate splicing of a single gene mapped to chromosome 8p. The two
major types, alpha and beta HRG's are based on two variant EGF-like
(epidermal growth factor) domains, that differ in their C-terminal ends.
This method can be used to increase the number of inner-ear-supporting
cells and for treatment of hair cell related hearing disorders and
disease states associated with tissue damage, e.g. octoxic injury,
acoustic assault, degenerative hearing loss, balance impairments, damage
associated with surgery or physical injury and inner ear disorders
related to hair cell dysfunction. The present sequence is the human
related to hair cell dysfunction. The present sequence is the human
theregulin ligand, HRG-betal protein variant-21. Note: This sequence is
equence found in the specification and is derived from the HRG-betal protein
sequence found in Figure 2 (AAX71172)
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HRG-betal mature
                                                                                                                                                                                                                           Heregulin; HRG betal; human; mutant; mutein; inner-ear-supporting cell; activator; HER2 receptor; HER3 receptor; HER-2 oncogene; chromosome 8p; hair cell related hearing disorder; ototoxic injury; tissue damage; acoustic assault; degenerative hearing loss; balance impairment; treatment; surgical injury; physical injury; inner ear disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Method for inducing hair cell generation and inner-ear-supporting ogrowth regeneration and proliferation, useful for treating hearing disorders.
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Score 3344; DB 3; Pred. No. 3.6e-204;

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Query Match Best Local Similarity

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Misc-difference 225
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Misc-difference 31
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Synthetic.
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/note= "Wild type Phe replaced with Tyr; This variable site corresponds to position 197, of the HRG-betal mature protein, after initiatior Met (M31)"
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                                                                                        RPLILVTPPRIREKKFDHHPQQFSSFHHNPAHDSNSLPASPLRIVEDESYETTQEYEPAQ
                                                                                                                                            EPVXXXLANSRRAKRTKPNGHIANRLEVDSNTSSQSSNSESETEDERVGEDTPFLGIQNPL
                                                                                                                                                                     EPVKKLANSRRAKRIKPNGHIANRLEVDSNISSQSSNSESETEDERVGEDIPFLGIONPL
                                                              RPLLLVTPPRLREKKFDHHPQQFSSFHHNPAHDSNSLPASPLRIVEDEEYETTQEYEPAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heregulin; HRG betal; human; mutant; mutein; inner-ear-supporting ce activator; HRR2 receptor; HRR3 receptor; HRR-2 oncogene; chromosome hair cell related hearing disorder; ototoxic injury; tissue damage; accustic assault; degenerative hearing loss; balance impairment; treatment; surgical injury; physical injury; inner ear disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hair cell generation and inner-ear-supporting and proliferation, useful for treating hearing
                                                                                                                                                                                                                 AASLEATPAFRLADSRINPAGRFSTQEELQARLSSVIANQDPIAV 645
                                                                                                                                                                                                                                                 AASLEATPAFRIADSRTNPAGRFSTQEEIQARLSSVIANQDPIAV
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Pred. No. 3.6e-204;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                   English.
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Matches 644; Conservative
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                                                                                                                                                                              (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                   Method for inducing growth regeneration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 675 AA;
                  WO200027426-A1
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acoustic assault, degenerative hearing loss, balance impairments, damage associated with surgery or physical injury and inner ear disorders related to hair cell dysfunction. The present sequence is the human heregulin ligand, HRG-betal protein variant-12. Note: This sequence is not found in the specification and is derived from the HRG-betal protein sequence found in Figure 2 (AAY71172)
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                                                                                                                                     Score 3344; DB 3;
Pred. No. 3.6e-204;
1; Mismatches 0;
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                                                                                                        Sequence 675 AA;
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The patent discloses a method for inducing hair cell generation, or inner car-supporting cell growth, regeneration, and/or proliferation, by halfold the ligand for HERZ-HERS dimeric receptors. Hergulin proteins function as activators of HER-2 oncogene and result from a lternate splicing of a single gene mapped to chromosome Bp. The two major types, alpha and beta HRG's are based on two variant EGF-like (epidermal growth factor) domains, that differ in their C-terminal ends. This method can be used to increase the number of inner-ear-supporting cells and for treatment of hair cell related hearing disorders and disease states associated with tissue damage, e.g. octooxic injury, counstic assault, degenerative hearing loss, balance impairments, damage associated with surgery or physical injury and inner ear disorders related to hair cell dysfunction. The present sequence is the human heregulin ligand, HRG-betal protein variant-14. Note: This sequence is
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                                                                                                               /note= "Wild type Lys replaced with Arg; This variable site corresponds to position 200, of the HRG-betal mature protein, after initiatior Met (M31)"
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Pred. No. 3.6e-204;
                                                                                    label= Initiator_methionine
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            Homo sapiens.
Synthetic.
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The patent discloses a method for inducing hair cell generation, or inner car-supporting cell growth, regeneration, and/or proliferation, by heregulins (HRG), the ligand for HREY-HRES dimeric receptors. Heregulin proteins function as activators of HRR-2 oncogene and result from alternate splicing of a single gene mapped to chromosome 8p. The two major types, alpha and beta HRG's are based on two variant EGP-like (epidermal growth factor) domains, that differ in their C-terminal ends. This method can be used to increase the number of inner-ear-supporting cells and for treatment of hair cell related hearing disorders and disease states associated with tissue damage, e.g. ottoxic injury, acoustic assault, degenerative hearing loss, balance impairments, damage associated with surgery or physical injury and inner ear disorders related to hair cell dysfunction. The present sequence is the human heregulin ligand, HRG-betal protein variant-5. Note: This sequence is not sequence found in Figure 2 (AAY71172)
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Pred. No. 4.1e-204;
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420 450 540

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206 of (M31)"
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/note= "This variable site corresponds to position 206
the HRG-betal mature protein, after initiatior Met (M31
                                                                                                                                211 KCAEKEKTFCVNGGECFWVKDLSNYLCKCPNEFTGDRCQNYVIASFYKHLGIEFMEA
                                                                                                                                                                                                                        EELYQKRVLTITGICIALLVVGIMCVVAYCKTKKQRKKLHDRLRQSLRSERNNMMNIANG
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                                                                 DSASANITIVESNEIITGMPASTEGAYVSSESPIRISVSTEGANTSSSTSTSTTGTSHLV
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                                                                                                              KCAEKEKTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCQNYVMASFYKHLGIEFMEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Heregulin HRG-betal protein variant-17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The patent discloses a method for inducing hair cell generation, or inner ear-supporting cell growth, regeneration, and/or proliferation, by heregulins (HRG), the ligand for HERZ-HERS dimeric receptors. Heregulin proteins function as activators of HER-2 oncogene and result from alternate splicing of a single gene mapped to chromosome 8p. The two major types, alpha and bete HRG's are based on two variant EGF-like (epidermal growth factor) domains, that differ in their C-terminal ends. This method can be used to increase the number of inner-ear-supporting cells and for treatment of hair cell related hearing disorders and disease states associated with tissue damage, e.g. ottoxic injury, associated with surgery or physical injury and inner ear disorders related to hair cell dysfunction. The present sequence is the human the specification in variant-26. Note: This sequence is not found in the specification and is derived from the HRG-betal protein content of the HRG-betal protein variant-26. Note: This sequence is
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HRG-betal mature
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                                                                                                                            Heregulin; HRG betal; human; mutant; mutain; inner-ear-supporting cell; activator; HER2 receptor; HER3 receptor; HER-2 oncogene; chromosome 8p; hair cell related hearing disorder; ottochoxic injury; tissue damage; acoustic assault; degenerating hose; balance impairment; treatment; surgical injury; physical injury; inner ear disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Method for inducing hair cell generation and inner-ear-supporting or growth regeneration and proliferation, useful for treating hearing disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Wild type Met replaced with Ile;
site corresponds to position 226, of the
protein, after initiatior Met (M31)"
                                                                                     Human Heregulin HRG-betal protein variant-26,
                                                                                                                                                                                                                                                                                                                                                                      /label= Initiator_methionine
                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                          (first entry)
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Best Local Similarity 99.8
Matches 644; Conservative
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AAY71203;
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571 EPVKKLANSRRAKRTKPNGHIANRLEVDSNTSSQSSNSESETEDERVGEDTPFLGIQNPL 630
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AAY7180
AAY71180
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                                                                                                                                                                                                                                                                                                                                                                rear-supporting cell growth, regeneration, and/or proliferation, by heregulins (HRG), the ligand for HRS2/HER3 dimeric receptors. Heregulin alternate splicing of a single gene mapped to chromosome Bp. The two major types, alpha and beta HRG's are based on two variant EGF-like (epidermal growth factor) domains, that differ in their C-terminal ends. This method can be used to increase the number of inner-ear-supporting cells and for treatment of hair cell related hearing disorders and disease states associated with fissue damage, e.g. ototoxic injury, accoustic assoult, degenerative hearing loss, balance impairments, damage associated with surgery or physical injury and inner ear disorders related to hair cell dysfunction. The present sequence is the human regulant ligand, HRG-betal protein variant-17. Note: This sequence is not found in the specification and is derived from the HRG-betal protein sequence from the HRG-betal protein sequence is not found in Figure 2 (AAY71172)
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                                                                                                                                                                                                                                                                                                                                            patent discloses a method for inducing hair cell generation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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Pred. No. 4.1e-204;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                    English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 99.8
Matches 644; Conservative
                                                                                                                                                                                                                                                                                       Page; 141pp;
(GETH ) GENENTECH INC.
                                                                                                               WPI; 2000-376313/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 675 AA;
                                                                                                                                                                                                                                                                                    Disclosure;
                                                                                                                                                                 Method for growth reg disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            331
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The patent discloses a method for inducing hair cell generation, or inner ear-supporting cell growth, regeneration, and/or proliferation, by heregulins (HRG), the ligand for HRE2/HRE3 dimeric receptors. Heregulin proteins function as activators of HER-2 oncogene and result from a lternate splicing of a shaple gene mapped to chromosome 8p. The two major types, alpha and beta HRG's are based on two variant EGF-like (epidermal growth factor) domains, that differ in their C-terminal ends. This method can be used to increase the number of inner-ear supporting cells and for treatment of hair cell related hearing disorders and disease states associated with tissus damage, e.g. otocoxic injury, associated with surgery or physical injury and inner ear disorders related to hair cell dysfunction. The present sequence is the human the regulin ligand, HRG-betal protein variant-3. Note: This sequence is not found in Figure 2 (AAY71172)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= Gln, 11e, Glu
/note= "This variable site corresponds to position 180 of
the HRG-betal mature protein, after initiatior Met (M31)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heregulin; HRG betal; human; mutant; mutein; inner-ear-supporting cell; activator; HER2 receptor; HER3 receptor; HER-2 oncogene; chromosome 8p; hair cell related hearing disorder; ototoxic injury; tissue damage; acoustic assault; degenerative hearing loss; balance impairment; treatment; surgical injury; physical injury; inner ear disorder.
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AASLEATPAFRLADSRINPAGRFSTQEEIQARLSSVIANQDPIAV
                                        AASLEATPAFRLADSRTNPAGRFSTQEEIQARLSSVIANQDPIAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human Heregulin HRG-betal protein variant-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                      AAY71180 standard; protein; 675 AA.
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Synthetic.
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disorders.
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0,	09	90	120	150	180	210	240	270	300	330	360	390	420	450	480	510	540	570	009	630		
99.9%; Score 3342; DB 3; Length 675; Similarity 99.8%; Pred. No. 4.8e-204; 4; Conservative 0; Mismatches 1; Indels 0; Gaps	MSERKEGRGKGKKKKERGSGKKPESAAGSQSPALPPQLKEMKSQESAAGSKLVLRCETS	MSERKEGRGKGKGKKKERGSGKKPESAAGSQSPALPPQLKEMKSQESAAGSKLVLRCETS	SEYSSLRFKWFKNGNELNRKNKPQNIKIQKKPGKSELRINKASLADSGEYMCKVISKLGN	SEYSSLRFKWFKWGWELNRKNKPQWIKIQKKPGKSELRINKASLADSGEYMCKVISKLGN	DSASANITIVESNEIITGMPASTEGAYVSSESPIRISVSTEGANTSSSTSTSTTGTSHLV	DSASANITIVESNEIITGMPASTEGAYVSSESPIRISVSTEGANTSSSTSTSTTGTSHLI	KCAEKEKTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCQNYVMASFYKHLGIEFMEA	KCAEKEKTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCQNYVMASFYKHLGIEFMEA	BELYQKRVLTITGICIALLVVGIMCVVAYCKTKKQRKKLHDRLRQSLRSERNNMMIANG	BELYQKRVLTITGICIALLVVGIMCVVAYCKTKKQRKKLHDRLRQSLRSERNNMMIANG	PHHPNPPPENVQLVNQVVSKNVISSEHIVEREAETSFSTSHYTSTAHHSTTVTQTPSHSW	PHHPPPPENVQLVNQYVSKNV1SSEHIVEREAETSFSTSHYTSTAHHSTTVTQTPSHSW	SNGHTESILSESHSVIVMSSVENSRHSSPTGGPRGRLNGTGGPRECNSFLRHARETPDSY	SNGHTESILSESHSVIVMSSVENSRHSSPTGGPRGRINGTGGFRECNSFLRHARETPDSY	RDSPHSERYVSAMTTPARMSPVDFHTPSSPKSPPSEMSPPVSSMTVSMPSMAVSPFMEE	RDSPHSERYVSAMTTPARMSPVDFHTPSSPKSPPSEMSPPVSSMTVSMPSMAVSPFMEEE	RPLLLVTPPRLREKKFDHHPQQFSSFHHNPAHDSNSLPASPLRIVEDEEYETTQEYEPAQ	RPLLLVTPPRLREKKFDHHPQPFSSFHHNPAHDSNSLPASPLRIVEDEEYETTQEYEPAQ	EPVKKLANSRRAKRTKPNGHIANRLEVDSNTSSQSSNSESETEDËRVGEDTPFLGIQNPL	EPVKKLANSRRAKRTKPNGHIANRLEVDSNTSSQSSNSESETEDERVGEDTPFLGTQNPL	AASLEATPAFRLADSRTNPAGRFSTQEELQARLSSVIANQDPIAV 645	AASLEATPAFRLADSRINPAGRESTQEBIQARLSSVIANQDPIAV 675
Match Local es 64	rd	31	61	16	121	151	181	211	241	271	301	331	361	391	421	451	481	511	541	571	601	631
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Search completed: April 12, 2005, 14:30:39 Job time : 183 secs

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Sequence

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Scoring table:

Searched:

Database

Result No.

Perfect score:

Sequence:

OM protein

Run on:

Sequence Sequence Sequence

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Length 645;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/847,743B
FILING DATE: 19920306
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705256
FILING DATE: 24-May-1991
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/765212
FILING DATE: 25-Sep-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/79801
FILING DATE: 08-No. 5367060-1991
ATTORNEY AGENT INFORMATION:
NAME: HORGEL AND AND NAME: HORGEL AND NAME HORGEL A
                  PCT-US92-04295A-28

US-08-467-662-274

US-08-467-662-264

US-08-411-295F-190

US-08-411-295F-190

US-08-411-295F-193

US-08-411-295F-193

US-08-467-662-267

US-08-467-662-268

US-08-467-662-268

US-08-467-662-268

US-08-467-662-268

US-08-467-662-268

US-08-467-662-268

US-08-467-662-256

US-08-467-662-354

US-08-467-662-354

US-08-467-662-354

US-08-467-662-354
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REGISTRATION NUMBER: 27,043
REFRENCE/DOCKET NUMBER: 712P3
TELECOMMUNICATION INPORMATION:
TELEPHONE: 415/266-1489
TELEX: 910/371-7168
INPORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
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TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inc
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7, Appl
                                                                                                                                                                                        April 12, 2005, 14:27:47 ; Search time 43 Seconds (without alignments) 1119.736 Million cell updates/sec
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Sequence 4, Appli
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Sequence 10, 7
Sequence 270,
Sequence 196,
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(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                     GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-428-27-4
US-08-329-217-4
US-08-456-241-27
US-09-020-880-93
US-09-101-544-93
US-09-097-681-3
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US-08-467-602-270
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US-08-456-241-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                          - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                          US-10-082-747A-93
3347
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Match Length
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181 KCAEKEKTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONYVMASFYKHLGIEFMEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DSASANITIVESNEIITGMPASTEGAYVSSESPIRISVSTEGANTSSSTSTSTTGTSHLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 100.0%; Score 3347; DB 1; Best Local Similarity 100.0%; Pred. No. 1.3e-244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                        US/08/126,145
                                                                        FILING DATE: 07/06/22/17/18/18/19/19/24/19/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24/19/24
                                                                                                                                                                                                                                                                                                                                         27,034
ER: 712P4
                                                                                                                                                                                                                                                                                                              NAME: Heneley, Max D.
REGISTRATION NUMBER: 27,034
REFERENCE/DOCKET NUMBER: 712P-
TELECOMMUNICATION INFORMATION:
TELEPAX: 415/266-1489
TELEX: 910/311-7168
INPORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 645 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 645; Conservative
                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                  SEYSSLRFKWFKNGNELNRKNKPQNIKIQKKPGKSELRINKASLADSGEYMCKVISKLGN 120
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                                                                           1 MSERKEGRGKGKKKKERGSGKKPESAAGSQSPALPPQLKEMKSQESAAGSKLVLRCETS
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APPLICANT: Vandlen, Richard L.,
APPLICANT: Vandlen, William E.
ITILE OF INVENTION: Structure, Production and Use of
ITILE OF INVENTION: Heregulin 2 Ligands
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                           Indels
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  Pred. No. 1.3e-244;
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COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,201
FILING DATE:
                           0; Mismatches
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Patent No. 5641869
100.08;
                           645; Conservative
Best Local Similarity
Matches 645; Conserv
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US-08-456-201-27
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Length Indels 180

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                        361 SNGHTESILSESHSVIVMSSVENSRHSSPTGGPRGRLNGTGGPRECNSFLRHARETPDSY
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                                                                                 RDSPHSERYVSAMTTPARMSPVDFHTPSSPKSPPSEMSPVSSMTVSMPSMAVSPFMEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08428927

Ratent No. 5756456

GENERAL INFORMATION:
APPLICANT: Ho, Wel-Hsien
APPLICANT: Osheroff, Phyllis L.
TITLE OF INVENTION: SENSORY AND MOTOR NEURON DERIVED FACTOR (SMDF)
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 3347; DB 1; Length 645; 100.0%; Pred. No. 1.3e-244; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                         AASLEATPAFRLADSRTNPAGRFSTQEEIQARLSSVIANQDPIAV 645
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ZIP: 94080-
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
MEDIUM TYPE: 5.25 ompatible
TYPE: DC-DOS/MS-DOS
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SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,927
FILING DATE: 25-APR-1995
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION WHERE: 08/339517
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lee, WendY M.
REGISTRATION NUMBER: 00,000
REGISTRATION NUMBER: 00,000
REGISTRATION NUMBER: 853D3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 460 Point San Bruno Blvd CITY: South San Francisco STATE: California
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amino acid
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
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Matches 645; Conservative
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LENGTH: 645 amino aci
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; Pred. No. 1.3e-244;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                      ZIP: 94080
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: 1BM FC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,926
FLING DATE: 25-APR-1995
CLASSIFICATION DATE: 25-APR-1995
FLING APPLICATION DATE: 35-APR-1995
FLING APPLICATION DATE: 18-NOV-1994
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                      APPLICANT: Ho, Wei-Hsien
APPLICANT: Osheroff, Phyllis L.
TITLE OF INVENTION: SENSORY AND MOTOR
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 00,000
REGISTRATION NUMBER: 00,000
REFRENCE DOCKET NUMBER: 853D4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415,952.9881
                                                                             Sequence 4, Application US/08428926
Patent No. 5667780
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
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Best Local Similarity
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TOPOLOGY: linear
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                                                             US-08-428-926-4
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| TELEPHONE: 415/225-1994
| TELEFAX: 415/952-9881
| TELER: 910/371-7168
| INFORMATION FOR SEQ ID NO: 4:
| SEQUENCE CHARACTERISTICS:
| LENGTH: 645 amino acids
| TYPE: amino acids
| TOPOLOGY: linear
| US-08-428-298-4
                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 645; Conservative
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US-08-339-517-4
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DSASANITIVESNEIITGMPASTEGAYVSSESPIRISVSTEGANTSSSTSTSTTGTSHLV 180
                                                     KCAEKEKTPCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCQNYVMASFYKHLGIEFMEA 240
                                                                                                                   240
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                                                                                                                                           EELYQKRVLTITGICIALLVVGIMCVVAYCKTKKQRKKLHDRLRQSLRSERNNMMNIANG 300
                                                                                                                                                                                             PHHPNPPPENVQLVNQYVSKNVISSEHIVEREAETSFSTSHYTSTAHHSTTVTQTPSHSW 360
                                                                                                                                                                                                                                                                                                 RDSPHSERYVSAMTTPARMSPVDFHTPSSPKSPPSEMSPPVSSMTVSMPSMAVSPFMEEE 480
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                                                                                                       SNGHTESILGESHSVIVMSSVENSRHSSPTGGPRGRLNGTGGPRECNSFLRHARETPDSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   601 AASLEATPAFRLADSRTNPAGRFSTQEEIQARLSSVIANQDPIAV 645
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MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: 5.25 inch, 360 Kb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,298
FILING DATE: 25-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/339517
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08428298
Patent No. 5762131
GENERAL INFORMATION:
APPLICANT: Ho, Wal-Hsien
APPLICANT: Osheroff, Phyllis L.
TITLE OF INFORMION: SENSORY AND MOS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
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STREET: 460 Point San Bruno I
CITY: South San Francisco
STATE: California
COUNTRY: USA
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REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 853
TELECOMMUNICATION INFORMATION:
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US-08-428-298-4
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                                                                                                                                              1 MSERKEGRGKGKGKKKERGSGKKPESAAGSQSPALPPQLKEMKSQBSAAGSKLVLRCETS
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Length 645;
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100.0%; Score 3347; DB 1;
100.0%; Pred. No. 1.3e-244;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Ho, Wei-Heien
APPLICANT: OSheroff, Phyllis L.
TITLE OF INVENTION: SENSORY AND MOTO
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Generacch, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08339517
Patent No. 5770567
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61 SEYSSLRFKWFKNGNELNRKNKPQNIKIQKKPGKSELRINKASLADSGEYMCKVISKLGN 120
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                            601 AASLEATPAFRLADSRTNPAGRFSTQEEIQARLSSVIANQDPIAV
                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Vandlen, Richard L.
APPLICANT: Holmes, William E.
TITLE OF INVENTION: STRUCTURE, PRODUCTION AND USE OF
TITLE OF INVENTION: HEREGULIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZUDINITE SADDABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PALING DATA: PC-DOS/MS-DOS SOFTWARE: PALING DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/08/456,241

FILING DATE: 31-MAY-1995

FRION APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: 09/126145

FILING DATE: 23-SEP-1993

FRION APPLICATION DATA: APPLICATION NUMBER: 07/840917

FILING DATE: 06-MAX-1992

FRION APPLICATION NUMBER: 07/941743

FILING DATE: 06-MAX-1992

FRION APPLICATION DATA: APPLICATION NUMBER: 07/765212

FILING DATE: 25-SEP-1991

PRION APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: 07/765212

FILING DATE: 25-SEP-1991

PRION APPLICATION DATA: APPLICATION NUMBER: 07/705256

FILING DATE: 24-MAY-1991
                                                                                                                                                                                                                                                                                                                       STREET: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                          Sequence 27, Application US/08456241
Patent No. 5840525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELER: 910/371-7168
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
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REFERENCE/DOCKET NUMBER:
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Matches 645; Conservative
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                                                                  5.25 inch, 360 Kb floppy disk
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                                                                                                                                                                        APPLICATION NUMBER: US/08/339,517
FILING DATE: 14-NOV-1994
CLASSPRICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTONEN'AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 853
TELECHOME: 415/225-1994
TELEFRX: 415/952-9881
                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/339,5:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 in
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Best Local Similarity
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COUNTRY:
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181 KCAEKEKTFCVNGGECFWVKDLSNPSRYLCKCPNEFTGDRCQNYVMASFYKHLGIEFMEA 240
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                          61 SEYSSLRFKWFKNGNELNRKNKPQNIKIQKKPGKSELRINKASLADSGEYMCKVISKLGN
                                                                       PHHPNPPPENVQLVNQYVSKNVISSEHIVEREAETSFSTSHYTSTAHHSTTVTQTPSHSW
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APPLICANT: Ballinger, Marcus D.
APPLICANT: Ballinger, Marcus D.
APPLICANT: Ballinger, Marcus D.
APPLICANT: Fairbrother, Wayne J.
APPLICANT: Sliwkowski, Mark X.
APPLICANT: Sliwkowski, Mark X.
APPLICANT: Wells, James A.
TITLE OF INVENTION: HERECULIN VARIANTS
FILE REFERENCE: 14918-720CON2
CURRENT APPLICATION NUMBER: US/09/101,544
CURRENT FILING DATE: 1998-07-17
PRIOR APPLICATION NUMBER: US 60/037,581
PRIOR FILING DATE: 1998-02-09
PRIOR FILING DATE: 1997-02-10
NUMBER OF SEQ ID NOS: 116
SEQ ID NOS: 116
SEQ TWARKE: FASELSEQ for Windows Version 4.0
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; ORGANISM: Homo sapiens
US-09-101-544-93
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.larity 100.0%; Pred. No. 1.3e-244;
Conservative 0; Mismatches 0;
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APPLICANT: Genentech, Inc.
APPLICANT: Genentech, Inc.
APPLICANT: Genentech, Inc.
APPLICANT: Ballinger, Marcus D.
APPLICANT: Jones, Jennifer T.
APPLICANT: Sliwkowski, Mark X.
APPLICANT: Sliwkowski, Mark X.
APPLICANT: Sliwkowski, Mark X.
APPLICANT: Wells, James A.
TILE OF INVENTION: HEREGULIN VARIANTS
FILE REFERENCE: 14918-720CON1
CURRENT APPLICATION NUMBER: US/09/020,880A
CURRENT FILING DATE: 1997-02-09
BARLIER APPLICATION NUMBER: US 60/037,581
EARLIER FILING DATE: 1997-02-10
NUMBER OF SEQ ID NOS: 116
SCOTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 93
LENGTH: 645
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1×.09-020-880-93
Sequence 93, Application US/09020880A
Patent No. 6136558
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US-09-020-880-93
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100.0%; Pred. No. 1.3e-244;
tive 0; Mismatches 0;
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7-1092-04295A-27

Sequence 27, Application PC/TUS9204295A

GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
TITLE OF INVENTION: Structure, Prodition of INVENTION: Heregulin
                                                                              PF383PCT
                                  NAME: HOOVET, KEALLEY K.
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PF383
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-6439
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 645 amino acids
TYPE: amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPPICATION
   FILING DATE: 17-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hoover, Kenley K.
                                                                                                                                                                                                                                                                                                                                                        Matches 645; Conservative
                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
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Best Local Similarity
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                                                         SEYSSLRFKWFKNGNELNRKNKPQNIKIQKKPGKSELRINKASLADSGEYMCKVISKLGN 120
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                                                                                                                                                                                                                               EELYQKRVLTITGICIALLVVGIMCVVAYCKTKKQRKKLHDRLRQSLRSERNNMMNIANG
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SNGHTESILSESHSVIVMSSVENSRHSSPIGGPRGRLNGTGGFRECNSFLRHARETPDSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Young, Paul
APPLICANT: King, C. Richter
APPLICANT: Hijazi, Mai
APPLICANT: Ruben, Steve
TITLE OF INVENTION: Heregulin-Like Fac
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc
STREET: 9410 Key West Avenue
CITY: Rockville
CITY: Nockville
STATE: MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20850
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
PROR APPLICATION DATA:
APPLICATION NUMBER: US 60/049,942
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US-09-097-681-3
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                                                                                                                                     481 RPLLLYTPPRLREKKFDHHPQQFSSFHHNPAHDSNSLPASPLRIVEDEEYETTQEYEPAQ 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9, Application US/07847743B
Patent No. 5367060
GENERAL INFORMATION:
FITLE OF INVENTION: Structure, Production and Use;
TITLE OF INVENTION: Heregulin
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STRATE: Couth San Francisco
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MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 1725050
CLIANG EACH 1 1725050
ERIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705256
FILING DATE: 24-May-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/765212
FILING DATE: 25-Sep-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/790801
FILING DATE: 08-No. 5367060-1991
ATTORNEY/AGENT INFORMATION:
NAME: Henelley, Max D.
REGISTRATION NUMBER: 27,043
REFERENCE/DOCKET NUMBER: 77,12P3
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/847,743B
FILING DATE: 19920306
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TELEFAX: 415/952-9881
TELEX: 910/317-718
INFORMATION FOR SEQ ID NO: 9:
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415/952-9881
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US-07-847-743B-9
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                                                                                                                                                                                                              ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: patin relevants
SOFTWARE: patin relevants
CURRENT APPLICATION DATA:
FILING DATE: 19920521
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION WINBER: 07/705256
FILING DATE: 24-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION WINBER: 07/765212
FILING DATE: 25-SEP-1991
PRIOR DATE: 08-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/790801
FILING DATE: 08-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/790801
FILING DATE: 08-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/790801
FILING DATE: 06-MAR-1992
ATTORNEY AGENT INFORMATION:
ANAME: USEN ANAME: NOT ANAME: N
                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 27,043
REGISTRATION NUMBER: 27,043
REFERENCE/DOCKET NUMBER: 712P-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/255-981
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 645 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
NUMBER OF SEQUENCES: 30
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Best Local Similarity
Matches 645; Conserval
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BELYQKRVLTITGICIALLVVGIMCVVAYCKTKKQRKKLHDRLRQSLRSERNNMMNIANG
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                             PRIOR APPLICATION DATE:
APPLICATION NUMBER: 07/705256
PRIOR APPLICATION NUMBER: 07/765212
PRIOR APPLICATION NUMBER: 07/765212
PRIOR APPLICATION NUMBER: 07/790801
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                     TOPOLOGY: linear
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                 MSERKEGRCKGKGKKKERGSGKKPESAAGSOSPALPPOLKEMKSOESAAGSKLVLRCETS
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MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IBM CCOMPATIBLE COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech) CURRENT APPLICATION NUMBER: US/08/456,201
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION 543
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/126,145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/08456201; Patent No. 5641869; GENERAL INFORMATION:
APPLICANT: Vandlen, Richard L.,
APPLICANT: Holmes, William E.; TITLE OF INVENTION: Structure, Production and; TITLE OF INVENTION: Heregulin 2 Ligands; NUMBER OF SEQUENCES: 3 CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc., STREET 460 Point San Bruno Blvd
CTTY: South San Francisco; STATE: California
COUNTRY: USA
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US-08-456-201-9
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COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: 1EM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/04295A
FILING DATE: 19920521
CLASSIFICATION:
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GENERAL INFORMATION:
FITTE OF INVENTION:
TITLE OF INVENTION: Berequin
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET 460 Point San Bruno Blvd
CITY: South San Francisco
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APPLICATION NUMBER: 07/705256
FILING DATE: 24 MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/765212
FILING DATE: 25-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/790801
FILING DATE: 08-NOV-1991
PRIOR APPLICATION NUMBER: 07/790801
FILING DATE: 06-MAR-1992
ATTORNEY/AGENT INFORMATION:
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100.0%; Score 3347; DB 2;
Best Local Similarity 100.0%; Pred. No. 1.6e-244;
Matches 645; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                          712P4C1D1
                                                                                                                                                                                                                                  ADDRESSEE: Generatech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSITION NUMBER: 943
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/126145
PRIUNG DATE: 23-SEP-1993
PRIUNG APPLICATION DATA:
APPLICATION NUMBER: 07/880917
PRIUNG DATE: 11-MAY-1992
PRIUNG DATE: 07-841992
PRIUNG DATE: 07-841992
PRIUNG DATE: 07/90801
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/790801
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/765212
PRIUNG DATE: 08-NOV-1991
PRIUNG DATE: 07-85-1991
PRIUNG DATE: 07-85-1991
PRIUNG DATE: 24-MAY-1991
ATTONNEY/AGENT INFORMATION:
NAME: Lee, Wenddy M:
NAME: NAME:
; Sequence 9, Application US/08456241
; Patent No. 5840525
; GENERAL INFORMATION:
    APPLICANT: Vandlen, Richard L. APPLICANT: Holmes, William E. TITLE OF INVENTION: HEREGULIN
    TITLE OF INVENTION: HEREGULIN
    NUMBER OF SEQUENCES: 30
    NUMBER OF SEQUENCES: 3
    ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 71
TELECOMMUNICATION INFORMATION:
TELEPAN: 415/952-1994
TELEFAX: 415/952-9881
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                  Indels
                                                                                                                                                      Query Match 100.0%; Score 3347; DB 5; Best Local Similarity 100.0%; Pred. No. 1.6e-244; Matches 645; Conservative 0; Mismatches 0;
REFERENCE/DOCKET NUMBER: 712P;
TELEPHONE: 415/225-1994
TELEPHONE: 415/252-1994
TELERAX: 910/371-7168
INPORMATION: FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
LENGTH: 732 amino acids
TYPE: AMINO ACID
TOPOLOGY: 1inear
PCT-US92-04295A-9
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Search completed: April 12, 2005, 14:43:38 Job time : 45 secs

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Q7rtv8
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P4332
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Q6DR99
Q9ESB1
Q9ESB0
NRG1 XENLA
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NRG2 MOUSE
NRG2 RAT
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NRG1 HUMAN
Q7RTV8
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Q9ESA1
NRG2 HUMAN
Q8BKI8
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Maximum Match 100%
Listing first 45 summaries
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Q6TGK9
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Q7RTV9
Q862K0
Q862K0
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 200000000
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3347
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       SMDF HUMAN
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## ALIGNMENTS

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61 SEYSSLRFKWFKNGNELNRKNKPQNIKIQKKPGKSELRINKASLADSGEYMCKVISKLGN 120
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Stefansson H., Sigurdsson E., Steinthorsdottir V., Bjornsdottir S., Sigurdsson B., Brynjolfsson J., Gunnarsdottir S., Sigurdsson O., Chou T.T., Hjaltason O., Birgisdottir B., Jonsson H., Gudnadottir V.G., Gudmundsdottir E., Bjornsson A., Ingvarsson B., Ingason A., Sigusson S., Hardardottir H., Harvey R.P., Brunner D., Mutel V., Gonzalo A., Lemke G., Sainz J., Johannesson G., Andresson T., Gudbjartsson D., Manolescu A., Frigge M.L., Gurney M.E., Kong A., Gulcher J.R., Petursson H., Stefansson K.; Am. J. Hum. Genet. 71:0-01(202).

-I- MISCELLANBOUS: The sequence shown here is derived from an EMBL/Genabank/DDBA third party annotation (TPA) entry.
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                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PROSITE; PSO0022; EGF 1; UNKNOWN 1.
PROSITE; PS50026; EGF 3; 1.
PROSITE; PS50035; IG LIKE; 1.
SEQUENCE 645 AA; 71126 MW; 0487AFF528CDD628 CRC64;
                                                                                                                                                           , Last sequence update)
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Pred. No. 3.3e-175;
1; Mismatches 1;
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645 AA
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PRT;
                                                                                                                                                                                                                                                                             Neuregulin 1 isoform HRG-betal
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                                                                                                 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26,
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PRELIMINARY;
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NRG21 HUMAN

NRG31 (212782; Q12783; Q12784; Q9UPE3;

16-OCT-2001 (Rel. 40, Last sequence update)

16-OCT-2001 (Rel. 45, Last amontation update)

Pro-neuregulin-1 precursor (Pro-NRG3) [Contains: Neuregulin-1 (Neu differentiation factor) (Heregulin) (HRG) (Breast cancer cell differentiation factor) (Heregulin) (HRG) (Breast cancer cell differentiation factor p45) (Acetylcholine receptor inducing activity) (ARIA) (Sensory and motor neuron-derived factor) (Glial growth
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                                                                                                                                                                              OB89DF6E2ED70333 CRC64;
                                                                                                                                                                                                               Score 3280; DB 2;
Pred. No. 4.4e-172;
1; Mismatches 1;
                                                                                                    PRINTS, PRO1089, NEUREGULIN, 1.
PROSITE; PS00022; EGF_1; UNKNOWN 1.
PROSITE; PS50005, EGF_3; 1.
PROSITE; PS500835; IG LIKE; 1.
SEQUENCE 637 AA; 70169 WW; 0B89
   InterPro, IPR006209, EGF like.
InterPro, IPR007110; Ig-like.
InterPro, IPR002154, Neuregulin.
Pfam; PF00008, EGF, 1.
Pfam; PF00047; Ig; 1.
Pfam; PF02158, Neuregulin; 1.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Last annotation update)
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GO; GO:0009790; P:embryonic development; IEA.
InterPro; IPR000742; EGF 2.
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01-WAR-2004 (TrEMBLrel. 26, Last seq
01-WAR-2004 (TrEMBLrel. 26, Last ann
Neuregulin 1 isoform HRG-betal.
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01-MAR-2004 (
01-MAR-2004 (
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Oncogene 18:5718-5721 (1999).
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  MEDIINE=99455251; PubMed=10523851; DOI=10.1038/sj.onc.1202950; Wang X.-Z., Jolicoeur E.M., Conte N., Chaffanet M., Zhang Y., Mozziconacci M.-J., Feiner H., Birnbaum D., Pebusque M.-J., Ron D.; "Gamma-heregulin is the product of a chromosomal translocation fusing the DOC4 and HGL/NRG1 genes in the MDA-MB-175 breast cancer cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Culouscou J.-M., Plowman G.D., Carlton G.W., Green J.M., Shoyab M.; "Characterization of a breast cancer cell differentiation factor that specifically activates the HRR4/pil80exb84 receptor."; J. Biol. Chem. 268:18407-18410(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                Levy R.B., Yarden Y.; "Isolation of the neu/HER-2 stimulatory ligand: a 44 kd glycoprotein that induces differentiation of mammary tumor cells.";
                                                                                             SEQUENCE FROM N.A. (ISOFORMS 1; 6; 7 AND 8), AND PARTIAL SEQUENCE. MEDLINE=92271253; PubMed=1350381; Holmes W.E., Sliwkowski M.X., Akita R.W., Henzel W.J., Lee J., Park J.W., Yansura D., Abadi N., Raab H., Lewis G.D., Shepard H.M., Kuang W.-J., Wood W.I., Goeddel D.V., Vandlen R.L.; Isoform ildentification of heregulin, a specific activator of p185erbB2."; Science 256:1205-1210(1992).
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=92208945; PubMed=1348215; DOI=10.1016/0092-8674(92)90131-U;
Peles E., Bacus S.S., Koski R.A., Lu H.S., Wen D., Ogden S.G.,
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MEDLINE=9472144; PubMed=9333014; DOI=10.1038/sj.onc.1201317;
Schaefer G., Fitzpatrick V.D., Sliwkowski M.X.;
"Gamma-heregulin: a novel heregulin isoform that is an autocrine growth factor for the human breast cancer cell line, MDA-MB-175.";
Oncogene 15:1385-1394(1997).
                                                                                                                                                                                                                                                     Wen D., Suggs S.V., Karunagaran D., Liu N., Cupples R.L., Luo Y., Janssen A.M., Ben-Baruch N., Trollinger D.B., Jacobsen V.L., Meng S.-Y., Lu H.S., Hu S., Chang D., Yang W., Yanigahara D., Koski R.A., Yanden Y.; as "Structural and functional aspects of the multiplicity of Neu differentiation factors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Brain;
MEDLINE=93126115; PubMed=8096067; DOI=10.1038/362312a0;
Marchionni M.A., Goodearl A.D.J., Chen M.S., Bermingham-McDonogh (Kirk C., Hendricks M., Danehy F., Misumi D., Sudhalter J., Kobayashi K., Wroblewski D., Lynch C., Baldasarre M., Hiles I., Davis J.B., Hsuan J.J., Totty N.F., Otsu M., McBurney R.N., Waterfield M.D., Stroobant P., Gwynne D.;
"Glial growth factors are alternatively spliced erbB2 ligands
                                   Eukaryota; Metazoa; Chordàta; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-210 FROM N.A.
Schoumacher F., Herzer S., Flury N., Kueng W., Mueller H.,
Eppenberger U.;
                                                Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. OF GAMMA-HEREGULIN FUSION PROTEIN.
                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS 2; 3; 4; 6; 7 AND 8). 
TISSUE=Kidney adenocarcinoma, and Pituitary;
MEDLINE=94158863; PubMed=7509448;
              Name=NRG1; Synonyms=GGF, HGL, HRGA, NDF, SMDF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORMS 8 AND 9).
                                                                                                                                                                                                                                                                                                                                         Mol. Cell. Biol. 14:1909-1919(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expressed in the nervous system.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 19-27.
MEDLINE=93366731; PubMed=7689552;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 362:312-318(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell 69:205-216(1992).
                             (Human)
                          Homo sapiens
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REDLYMB-00004L TRANSLOCKTION.

MEDLYMB-0005180; PubMed-10597312; DOI-10.1034/sj.onc.1203136;

MEDLYMB-0005180; PubMed-10597312; DOI-10.1034/sj.onc.1203136;

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us-10-082-747a-93.rup

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This SWISS-EROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                    -1. DISEASE: Involved in a rare t(8;11) chromosomal translocation that fuses the 5'end of OD24 to NRG1 (isoform 8). The product of this translocation was first thought to be an alternatively spliced isoform, called gamma-heregulin. Gamma-heregulin is a soluble activating ligand for the ERBB2-ERBB3 receptor complex and acts as an autocrine growth factor in a specific breast cancer cell line (MDA-WB-175). Not detected in Dreast carcinoma samples, including ductal, lobular, medullary, and mucinous histological types, neither in other breast cancer cell lines.
-!- SIMILARITY: Belongs to the neuregulin family.
-!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
                   of trafficking and proteolytic processing. Regulation of the proteolytic processing involves initial intracellular domain dimerization (By similarity).

DOMAIN: ERBB receptor binding is elicited entirely by the EGF-like
                                                                                                                                                                      -1- PTM: Extensive glycosylation precedes the proteolytic cleavage (By similarity).
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 DOMAIN: The cytoplasmic domain may be involved in the regulation
                                                                                                             PTM: Proteolytic cleavage close to the plasma membrane on the external face leads to the release of the soluble growth factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 3193.5; DB 1
Pred. No. 2.5e-167;
2; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (Se or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M94165; AAA58638.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA19950.1; -.
AAA19951.1; -.
AAA19952.1; -.
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AAA58640.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA19953.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             622; Conservative
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Matches 623
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As Stefansson H., Sigurdsson E., Steinthorsdottir V., Bjornsdottir S., R. Stefansson H., Sigurdsson E., Brynjolfsson J., Gunnarsdottir S., Indranson T., Ghosh S., Brynjolfsson J., Gunnarsdottir S., Indrason O., Chou T.T., Hjaltason O., Birgisdottir B., Jonsson H., Gudnadottir V.G., Gudmundsdottir E., Bjornsson A., Ingvarsson B., R. Ingason A., Sigusson S., Hardresson A., Frigge M.L., Bunner D., R. Andresson A., Frigge M.L., Gurney M.E., R. Andresson T., Gudbjartsson D., Manolescu A., Frigge M.L., Gurney M.E., R. Andresson T., Gudbjartsson D., Manolescu M., Frefansson K.; M. Guner, T.1:0-0(2002).

R. Andresson T., Gudbjartsson D., Manolescu A., Frigge M.L., Gurney M.E., R. Andresson T., Gudbjartsson D., Manolescu H., Frefansen K., Frefansson K.; M. J. Hum. Gener. T.1:0-0(2002).

R. MEL/GenBank/DDBJ third party annotation (TPA) entry.

EMBL/GenBank/DDBJ Ricceptor binding; IEA.

EMBL/GenBank/DDBJ Neuregulin.

EMBL/GenBank/DDBJ Neuregulin.

Efam; PPO0047; 19; 1.

EMBL/GenBank/DDBJ Neuregulin.

EMBL/GenBank/DDBJ Neuregulin.

EMBL/GenBank/DDBJ Neuregulin.
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NGHTESILSESHSVIVMSSVENSRHSSPTGGPRGRLNGTGGPRECNSFLRHARETPDSYR
                                                                             DSPHSERYVSAMTTPARMSPVDFHTPSSPKSPPSEMSPPVSSMTVSMPSMAVSPFMEEER
                                                                                                                                                          PLILVT PPRIREKKFDHHPQQFSSFHHNPAHDSNSLPASPLRI VEDEEYETTQEYEPAQE
                                                                                                                                                                                                                   PVKKLANSRRAKRTKPNGHIANRLEVDSNTSSQSSNSESETEDERVGEDTPFLGIONPLA
                                                                                                                                     PLLLVTPPRLREKKFDHHPQQFSSFHHNPAHDSNSLPASPLRIVEDEEYETTQEYEPAQE
                                                        DSPHSERYVSAMTTPARMSPVDFHTPSSPKSPPSEMSPPVSSMTVSMPSMAVSPFMEEER
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                                                                                                                                                                                                                                                                                                ASLEATPAFRLADSRINPAGRESTQEEIQARLSSVIANQDPIAV 645
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Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-WAR-2004 (TrEMBLrel. 26, Created)
01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Neuregulin 1 isoform HRG-alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                        640 AA
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PRO1089; NEUREGULIN.
PROSITE; PSO122; EGF 1; 1.
PROSITE; PSO1186; EGF 2; 1.
PROSITE; PS50026; EGF 3; 1.
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P43122; P43121; P43125; P43126; P43127; P43128;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2004 (Rel. 44, Last annotation update)
Pro-neuregulin-1 precursor (Pro-NRGI) [Contenins: Neuregulin-1 (Neu differentiation factor) [Heregulin] (HRG) (Acetylcholine receptor inducing activity) (ARIA) (Sensory and motor neuron-derived factor)
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                                                                                                                                                                                                                               Length 645;
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                                                                                                                                                                                               7E575AEF73F55047 CRC64;
                                                                                                                                                                                                                             94.1%; Score 3149; DB 2; 93.0%; Pred. No. 6.9e-165;
                                                                                                                                                                                                                                              ; Pred. No. 6.9e 21; Mismatches
               Pfam; PF00008; EGF; 1.
Pfam; PF00158; Neuregulin; 1.
Pfam; PF00158; Neuregulin; 1.
PRINTS; PR01089; NEUREGULIN.
SWART; SM00409; EGF; 1.
SWART; SM00409; EGF; 1.
PROSITE; PS50022; EGF; 1; UNKNOWN_1.
PROSITE; PS50025; EGF; 1; UNKNOWN_1.
EGF-like domain.
SEQUENCE 645 AA; 71381 MW; 7E575A
   InterPro; IPR002154; Neuregulin.
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Matches 600; Conservative
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                                SEYSSLRFKWPKNGNELNRKUKPQNIKIQKKPGKSELRINKASLADSGEYMCKVISKLGN
                                                                                              DSASANITIVESNEIITGMPASTEGAYVSSESPIRISVSTEGANTSSSTSTSTTGTSHLV
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                                                                                                                                                                                                                                                                                                                                                                                                                               RDSPHSERYVSAMTTPARMSPVDFHTPSSPKSPPSEMSPPVSSMTVSMPSMAVSPFMEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                RDSPHSERYVSAMTTPARMSPVDFHTPSSPKSPPSEMSPPVSSMTVSMPSMAVSPFMEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RPLLLLVTPPRLREKKFDHHPQQPSSFHHNPAHDSNSLPASPLRIVEDEEYETTQEYEPAQ
                                                                                                                                                               KCAEKEKTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCQNYVMASFYKHLGIEFMEA
                                                                                                                                                                                                                                                                                                                                                              SNGHTESILSESHSVIVMSSVENSRHSSPTGGPRGRLNGTGGPRECNSFLRHARETPDSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AASLEATPAFRLADSRTNPAGRFSTQEEIQARLSSVIANQDPIAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AASLEATPAFRLADSRTNPAGRFSTQEELQARLSSVIANQDPIAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Neuregulin-1 type I betal-a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
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InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C57/B16J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=Nrg1;
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Q6DR98;
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Q6DR98
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                               Name=BetA2A; Synonyma=NDF22;

IsoId=P43322-7; Sequence=VSP_003440;

Name=BetA3A; Synonyma=NDF4;

IsoId=P43322-7; Sequence=VSP_003438, VSP_003439;

IsoId=P43322-8; Sequence=VSP_00348, VSP_003439;

IsoId=P43322-8; Sequence=VSP_00348, VSP_003430;

In mesenchymal and nonneutronal organs. Betal is enriched in brain and stomach, in low amounts in the kidney, skin and heart and not detected in the liver, spleen, and placenta.

In Dow, IN The cytopasmic domain may be involved in the regulation of trafficking and proceolytic processing. Regulation of the protection of the protection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN: ERBB receptor binding is elicited entirely by the EGF-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTM: Proteolytic cleavage close to the plasma membrane on the external face leads to the release of the soluble growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- PTM: Extensive glycosylation precedes the proteolytic cleavage.-!- SIMILARITY: Belongs to the neurogulin family.
-!- SIMILARITY: Contains 1 EFF-like domain.
-!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
                                                                          IsoId=P43322-3; Sequence=VSP_003436, VSP_003443, VSP_003444;
                                                                                                                                                                                                                                                   Name=Beta2; Synonyms=NDF40;
IsoId=P43322-6; Sequence=VSP_003440, VSP_003441;
                                                                                                                                      IsoId=P43322-4; Sequence=VSP_003436,
                                                                                                                                                                                                             IsoId=P43322-5; Sequence=VSP_003437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, U02323, AAA19948.1; -.
EMBL, U02324, AAA19949.1; -.
EMBL, W92430; -; NOT_ANNOTATED_CDS.
PIR; I61718; I61719.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO1089; NEUREGULIN.
SMART; SM00181; EGF; 1.
PROSITE; PS00022; EGF 1; 1.
PROSITE; PS01186; EGF 2; FALSE_NEG.
PROSITE; PS01186; EGF 2; 1.
                                         Name=Alpha2B; Synonyms=NDF19
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InterPro; IPR002154; Neuregulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000742; EGF 2.
InterPro; IPR006209; EGF like.
InterPro; IPR006210; IEGF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U02315; AAA19940.1; -. EMBL; U02316; AAA19941.1; -. EMBL; U02317; AAA19942.1; -.
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Pfam; PF02158; Neuregulin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U02320; AAA19945.1
EMBL; U02321; AAA19946.1
EMBL; U02322; AAA19947.1
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EMBL; U02319; AAA19944.1
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   ***MEDLINE=98352096; PubMed=9685409; DOI=10.1074/jbc.273.32.20525;

***MEDLINE=98352096; PubMed=9685409; DOI=10.1074/jbc.273.32.20525;

***MEDLINE=98352096; PubMed=9685409; DOI=10.1074/jbc.273.32.20525;

***Transmembrane neurogulins interact with LIM kinase 1, a cytoplasmic protein kinase implicated in development of visuospatial cognition.";

***Latansmembrane neurogulins interact 19980;

***Lennerlow: 273:20525-20534(1998).**

***Lennerlow: 273:20525

***Lennerlow:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      region of LIMKi.
-1- SUBCELLIAR LOCATION: Exists as a type I membrane protein and as a proteolytically released soluble growth factor form. The membrane-bound form does not seem to be active.
                                 Name=Nrg1; Synonyms=Ndf;
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Neu differentiation factor: a transmembrane glycoprotein containing an EGF domain and an immunoglobulin homology unit."; Cell 69:559-572(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Levy R.B., Yarden Y., "Isolation of the neu/HER-2 stimulatory ligand: a 44 kd glycoprotein that induces differentiation of mammary tumor cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=92257596; Pubmed=1349853; DOI=10.1016/0092-8674(92)90456-M; Wen D., Peles E., Cupples R., Suggs S.V., Bacus S.S., Luo Y., Trail G., Hu S., Silbiger S.M., Levy R.B., Koski R.A., Lu H.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 14-36.
MEDLINE-92208945; PubMed=1348215; DOI=10.1016/0092-8674(92)90131-U;
Peles E., Bacus S.S., Koski R.A., Lu H.S., Wen D., Ogden S.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The cytoplasmic domain interacts with the LIM domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM ALPHA2C/NDF44), AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGULATION OF PROCESSING (ISOFORM ALPHA2C/NDF44).
MEDLINE=99069430; PubMed=9852099; DOI=10.1074/jbc.273.51.34335;
Liu X., Hwang H., Cao L., Wen D., Liu N., Graham R.M., Zhou M.;
"Release of the neuregulin functional polypeptide requires its
cytoplasmic tail.";
                                                                                                                                                                                                                                                                             Event=Alternative splicing; Named isoforms=8;
Comment=Additional isoforms seem to exist;
Name=Beta4; Synonyms=NDF42A;
Isoid=P43322-1; Sequence=Displayed;
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . Biol. Chem. 273:34335-34340(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mol. Cell. Biol. 14:1909-1919(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERACTION WITH LIMK1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cell 69:205-216(1992).
(Glial growth factor)]
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                                                                                                                                                                                   NCBI_TaxID=10116;
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540 RIVEDEEYETTQEYESVQEPVKKVTNSRRAKRIKPNGHIANRLEMDSNISSVSSNSESET
                                                                                                                                                                                                                                                                   301 LRQSLRSERSNLVNIANGPHPPPPFENVQLVNQVVSKNVISSEHIVEREVETSFSTSHY
                               TSTAMHSTTVTQTPSHSWSNGHTESILSESHSVIVMSSVENSRHSSPTGGPRGRLNGTGG
                                             SMIVSMPSMAVSPFMEEERPLLLVIPPRLREKKFDHHPQQFSSFHHNPAHDSNSLPASPL
                                                                                                                                                                                                                                                     EDERVGEDTPFLGIONPLAASLEATPAFRLADSRTNPAGRFSTQEEIQARLSSVIANQDP
                                                                                    PRECNSFLRHARETPDSYRDSPHSERYVSAMTTPARMSPVDFHTPSSPKSPPSEMSPPVS
                                                                                                                                                                                                RIVEDEEYETTQEYEPAQEPVKKLANSRRAKRTKPNGHIANRLEVDSNTSSQSSNSESET
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R.J. Jr.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-Sprague-Dawley; TISSUE-Spinal cord/brain stem;
Carroll S.L., Sconecypher M.S., Anderson K.D., Pearson R. Frohnert P.W.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databages.
-I- SIMILARITY: Contains 1 EGF-like domain.
EMBL; AF194993; AAG28433.1; --
HSSP; Q12780; 1HRE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86036 MW; F6174A68F4E27BDE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                            782 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Property Arrovatos; Neureguiin.
Pram; PP000008; EGF; 1.
Pram; PP00047; ig; 1.
Pram; PP02158; Neuregulin; 1.
PRINTS, RN0181; EGF; 1.
SWART; SW00181; EGF; 1.
SWART; SW00181; EGF; 1.
PROSITE; PS00022; EGF 1; UNKNOWN 1.
PROSITE; PS0025; EGF 1; UNKNOWN 1.
PROSITE; PS00589; PIS_HPR_SER; UNKNOWN 1.
PROSITE; PS00589; PIS_HPR_SER; UNKNOWN 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LRQSLRSERNNWANIANGPHHPNPPPENVQLVNQYVSKAVISSEHIVEREAETSFSTSHY 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DSASANITIVESNEIITGMPASTEGAYVSSESPIRISVSTEGANTSSSTSTTTGTSHLV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KCAEKEKTFCVNGGECFTVKDLSNPSRYLCKCPNEFTGDRCQNYVMASFYMTSRRRQET 240
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                                                                                                                                                                                             By similarity.

By similarity.

By similarity.

N-linked (GlCNAc. . .) (Potential).

N-linked (GlCNAc. . .) (Potential).

N-linked (GlCNAc. . .) (Potential).

PNETGDRCQUYVMASFYMTSRRKRQETEXFLERKLDHSLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YVSAMTTPPRÄMSPYDFHTPSSPKSPPSEMSPPVSSMTVS
-> HNLIAELRRNKAYRSKCMOIQLSATHLRPSSITHLGFI
L (in isoform Alpha2B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEYSSLRFKWPKNGNELNRKNKPQNIKIQKKPGKSELRINKASLADSGEYMCKVISKLGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MSERKEGRGKGKKKKERGSGKKPESAAGSQSPALPPQLKEMKSQESAAGSKLVLRCETS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MSERKEGRGKGKGKKKDRGSRGKPGPAEGDPSPALPPRLKEMKSQESAAGSKLVLRCETS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----KHLGIEFMEAEELYQKRVLTITGICIALLVVGIMCVVAYCKTKKQRKKLHDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KCAEKEKTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCQNYVMASFY------
                 protein sequencing; EGF-like domain;
Immunoglobulin domain; Multigene family;
                                                                   Pro-neuregulin-1, membrane-bound form.
Neuregulin-1.
Extracellular (Potential).
Internal signal sequence (Potential).
Cytoplasmic (Potential).
19-like C2-rype.
Ser/Thr-rich.
                                                                                                                                                                                                                                                                                             (in isoform
                                                                                                                                                                                                                                                                                                                                               WISRRKROETEKPLERKLDHSLVKESK -> KHLGIEFME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                         WISRRKRQETE -> STSTPFLSLPE (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Missing (In isoform Beta2 and isoform
                                                                                                                                                                                                                                                                                     KES -> QPGFTGARCTENVPMKVQTQE (in isoi Alpha2A, isoform Alpha2B and isoform Alpha2C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /FTIG=VSP 003440.
PPENVQ -> RVRTRG (in isoform Beta2)
/FTIG=VSP_003441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 662;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SP 003441.
(In isoform Alpha2C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Missing (In isoform Alpha2B) /Frid=VSP_003444.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 Missing (in isoform Beta3)./FTId=VSP 003439.
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                                                                                                                                                                                                                                                                                                                                                               (in isoform Betal).
/FIId=VSP_003437.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
91.4%; Score 3058.5; DB 1
Best Local Similarity 89.1%; Pred. No. 6.7e-160;
Matches 591; Conservative 25; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             003442.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      003443
                                                                                                                                                                                                                                                                                                                                    /FTId=VSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FTIG=VSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FTIG=VSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Missing
PS50835; IG LIKE; 1. ive splicing; Direct pein; Growth factor;
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               Alternative spl
Glycoprotein; C
Transmembrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 1), AND PARTIAL SEQUENCE.
STRANS-White Leghorn, TISSUE—Brain,
MEDINE—93201602; PubMed=8453670; DOI=10.1016/0092-8674(93)90407-H;
Falls D.L., Rosen K.M., Corfas G., Lane W.S., Fischbach G.D.;
"ARIA, a protein that stimulates acetylcholine receptor synthesis, is a member of the neu ligand family.";
cell 72:801-815(1993).
                                                                                199 SEYSSLRFKWFKNGNELNRKNKPENIKIQKKPGKSELRINKASLADSGEYMCKVISKLGN
                                                                                                                                                                                                         KCAEKEKTFCVNGGECFTVKDLSNPSRYLCKCPNEFTGDRCQNYVMASFYKHLGIEFMEA
                                                                                                                                                                                                                                                                                                                                      EELYQKRVLTITGICIALLVVGIMCVVAYCKTKKQRQKLHDRLRQSLRSERSNLVNIANG
                                                                                                                                                                                                                                                                                                                                                                                                  PHHPNPPPENVOLVNOYVSKNVISSEHIVEREVETSFSTSHYTSTAHHSTTVTOTPSHSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNGHTESVISESNSVIMMSSVENSRHSSPAGGPRGRIHGLGGPRD-NSFLRHARETPDSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            558 RDSPHSERYVSAMTTPARMSPVDFHTPSSPKSPPSEMSPVSSMTVSMPSVAVSPFVEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPVKKLANSRRAKRTKPNGHIANRLEVDSNTSSQSSNSESETEDERVGEDTPFLGIQNPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EPVKKYTNSRRAKRTKPNGHIANRLEMDSNTSSVSSNSESETEDERVGEDTPFLGIQNPL
                                                                                                                          SEYSSLRFKWFKNGNELNRKNKPQNIKIQKKPGKSELRINKASLADSGEYMCKVISKLGN
                                                                                                                                                                                       DSASANITIVESNEIITGMPASTEGAYVSSESPIRISVSTEGANTSSSTSTSTTGTSHLV
                                                                                                                                                                                                                                                     KCAEKEKTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCQNYVMASFYKHLGIEFMEA
                                                                                                                                                                                                                                                                                                                                                                                                                                              SNGHTESILSESHSVIVMSSVENSRHSSPTGGPRGRLNGTGGPRECNSFLRHARETPDSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RDSPHSERYVSAMTTPARMSPVDFHTPSSPKSPPSEMSPPVSSMTVSMPSMAVSPFMEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RPLLLVTPPRLREKKFDHHPQQFSSFHHNPAHDSNSLPASPLRIVEDEEYETTQEYEPAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   618 RPLLLVTPPRLREKKYDHHPQQLNSFHHNPAHQSTSLPPSPLRIVEDEEYETTQEYESVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oarius garius (mirche).
Eukaryota: Merazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                               Gaps
                               20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neuregulin-1
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                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NRG1 CHICK STANDARD; PRT; 602 AA. 005199; 073750; 073751; 073752; 16-0CT-2001 (Rel. 40, Last sequence update) 16-0CT-2001 (Rel. 44, Last annotation update) Pro-neuregulin-1 precursor (Pro-NRG1) [Contains: New (Acceylcholine receptor inducing activity) (ARIA)].
No. 1e-156;
                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORMS 2; 3 AND 4)
              Pred.
                                                           SGKKPESAAGSOSP
                            23;
             88.68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=NRG1; Synonyms=ARIA;
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chorda
                             579; Conservative
           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9031;
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                                                                    DOMAIN: ERBB receptor binding is elicited entirely by the EGF-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Extensive glycosylation precedes the proteolytic cleavage (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ED4) in both visceral and somatic motor neurons of spinal cord and is highest at ED6. Isoform 1 is not expressed until ED 6 in Spinal cord. At ED 11 both isoforms display comparable levels. DOMAIN: The cytoplasmic domain may be involved in the regulation of trafficking and proteolytic processing. Regulation of the proteolytic processing involves initial intracellular domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isoid=Q05199-4; Sequence=VSP 003445, VSP 003446, VSP 003447, VSP 003448; Note=The EGF-like domain is replaced by a cysteine-rich domain
            MEDLINE=98150951; PubMed=9491987; DOI=10.1016/S0896-6273(00)80454-7;
                                                                                                                                                                                                                                                                                                                                                                                by a cysteine-rich domain
                                                                                                                                                                                                                                                                                                                                                                                                                           VSP_003446;
by a cysteine-rich domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEVELOPMENTAL STAGE: Isoforms 2-4 are detected at embryonic day
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTM: Proteolytic cleavage close to the plasma membrane on the external face leads to the release of the soluble growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTM: Extensive glycosylation precedes the proteolytic clease similarity).
Similarity:
Similarity: Belongs to the neuregulin family.
SIMILARITY: Contains 1 EGF-like domain.
SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
                                          oŧ
                          Yang X., Kuo Y., Devay P., Yu C., Role L.; "A cysteine-rich isoform of neuregulin controls the level expression of neuronal nicotinic receptor channels during
                                                                                                                                                                                                                                                                                                                                 Note=Contains an Ig-like domain;
Name=2; Synonyms=CRD-NRG-BETAIA;
IsoId=Q05199-2; Sequence=VSP_003445;
Note=The EGF-like domain is replaced
                                                                                                                                                                                                                                                                                                                                                                                                           Name=3; Synonyms=CRD-NRG-BETA2A;
IsoId=Q05199-3; Sequence=VSP_003445,
Note=The EGF-like domain is replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synonyms=CRD-NRG-BETA2B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dimerization (By similarity).
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EGF like.
IEGF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L11264; AAA49037.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000742; E
InterPro; IPR006209; E
InterPro; IPR006210; I
InterPro; IPR007110; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A45769; A45769.
HSSP; Q12780; 1HRE.
                                                                                                                                                                                                                                                                                                                                                                                              (CRD);
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (RD)
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EMBL;
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SISTSTIGTSHLVKCAEKEKTFCVNGGECPMVKDLSNPSRYLCKCPNEFIGDRCQNYVMA 227
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         460
                                                                                                                                                                                                                                                                                                                                                                343 SRHTSPT-GPRGKLNGIGGPREGNSFLRHARETPDSYRDSPHSERYVSAMTTPARKSSPVD 401
                                                                                                                                                                                                                                                                                                                                     SSFHHNPAHDSNSLPASPLRIVEDEEYETTQEYEPAQEPVKKLANSRRAKRTKPNGHIAN 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                     RLEVDSNTSSQSSNSESETEDERVGEDTPFLGIQNPLAASLEATPAFRLADSRTNPAGRF 623
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                                                                                                                                                                                                                    FHTPSSPKSPPSEMSPPVSSMTVSMPSMAVSPFMEEERPLLLVTPPRLREKKFDHHPQQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76504 MW; 37D7928FD7D49AC9 CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Neuregulin-1 type III betal-a.
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PROSITE; PS50026; EGF3; 1.
EGF-11ke domain.
SEQUENCE 700 AA; 76504 MW; 37D7
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InterPro; IPR006209; EGF 1; InterPro; IPR006209; EGF 1; InterPro; IPR006210; IEGF.
InterPro; IPR00154; Neuregulin.
Pfam; PF00108; EGF; 1.
Pfam; PF01089; Neuregulin; 1.
PRINTS; PR01089; NEUREGULIN.
SWART; SM00181; EGF; 1.
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Extracellular (Potential).

Internal signal sequence (Potential).

Cytoplasmic (Potential).

Ig-like C2-type.

Ser/Thr-rich.

EGF-like.

By similarity.

By similarity.

By similarity.

By similarity.

N-linked (GlCNAC. . .) (Potential).

N-Linked (GLCNAC. . .) (Potential).
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ATETNLQTAPKLS (in isoform 2, isoform 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 ESAAGSQSPALPPQLKEMKSQESAAGSKLVLRCETSSEYSSLRFKWFKNGNELNRKNKPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NPPRYLCRCPNEFTGDRCQNYVMASFYKHLGIEFWEAEELYOKRVLTITGICIALLVVGI
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VSAMTTPARMSPVDFHTP -> HTPPTSLLLAGKVSLRVS
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                                                                           Pfam; PFC2158; Neureguiii, PRINTS; PR01089; NEUREGULIN.
PRINTS; PR01089; NEUREGULIN.
SWART; SW00181; EGF; 1.
SWART; SW000181; EGF; 1.
PROSITE; PS00186; EGF 2; FALSE_NEG.
PROSITE; PS0026; EGF 3; 1.
PROSITE; PS50026; EGF 3; 1.
PROSITE; PS50036; IG_LIKE; 1.
PROSITE; PS50036; IG_LIKE; 1.
Alternative splicing; Direct protein sequencing; EGF-like domain; Alternative splicing; Direct protein sequencing; EGF-like domain; Glycoprotein; Growth factor; Immunoglobulin domain; Transmembrane.
602 Pro-neuregulin-1, membrane-bound form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (In isoform 3 and isoform 4).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Missing (In isoform 4).
/FTId=VSP 003448.
4183C0E56CE5D346 CRC64;
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Id=VSP_003445.
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InterPro; IPR003598; Ig_c2.
InterPro; IPR002154; Neuregulin.
Pfam; PF00047; ig; 1.
Pfam; PF02158; Neuregulin; 1.
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196 ARTPEVRTPKSGTQPQTTETNLQTAPKLSTSTSTTGTSHLIKCAEKEKTFCVNGGECFTV
                                                               KDLSNPSRYLCKCPNEFTGDRCQNYVMASFYKHLGIEFMEAEELYQKRVLTITGICIALL
                                                                                                 KNVISSEHIVEREAETSFSTSHYTSTAHHSTTVTQTPSHSWSNGHTESILSESHSVIVMS
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Sciurognathi; Muridae; Murinae; Rattus.
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
8MDF neurogulin alpha 2a.
Name-Nrgl;
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PROSITE; PS01186; EGF 2; 1.
PROSITE; PS50026; EGF 3; 1.
EGF-11; PS00599; PTS_HPR_SER; UNKNOWN_1.
EGF-11; edomain.
SEQUENCE 695 AA, 75646 MW; 5277F2CBA2
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Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Rodentia,
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             RSERNNMMNIANGPHHPNPPPENVQLVNQYVSKNVISSEHIVEREAETSFSTSHYTSTAH
                                                                                                                                          HSTIVIQIPSHSWSNGHTESILSESHSVIVMSSVENSRHSSPIGGPRGRLNGIGGPRECN
                                                                                                                                                                        SFLRHARETPDSYRDSPHSERYVSAMTTPARMSPVDFHTPSSPKSPPSEMSPPVSSMTVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C STAANN=Sprague-Dawley;
C STRAIN=Sprague-Dawley;
C STAANN=Sprague-Dawley;
C STAANN=Sprague-Dawley;
L Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
1 - SIMILARITY: Contains 1 EGF-like domain.
EMBL; AF194189; AAG28427.1; - .
EMBL; AF194189; AAG28427.1; - .
EMBL; AF194189; ABG28427.1; - .
EMBL; AF194189; ABG28428; ABG28428; ABG28428; ABG28428; ABG28428; ABG28428; ABG28428, ABG28428; ABG28428; ABG78718; ABG78718;
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Last sequence update)
Last annotation update)
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29; Mismatches 52;
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                                                                                                                                                             SSEAYISPVSK-AQSEAGAHVIVQGDHAAVASEPSAVPIRKNRLSAFPPFHPIAPPFPSP
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                                                                                                                                                                                                                          IRI-SVSTEGANTSS-----STSTSTTGTSHLVKCAEKEKTFCVNGGECFMV
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MEDLINE=98352126; PubMed=968585; DOI=10.1016/S0169-328X(98)00085-0;
Yang J.F., Zhou H., Pun S., Ip N.Y., Peng H.B., Teim K.W.K.;
"Cloning of CDNAs encoding xenopus neuregulin: expression in myotomal muscle during embryo development.";
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MEDLINE=99316087; PubMed=10383827; DOI=10.1006/mcne.1999.0759;
Yang J.F., Zhou H., Choi R.C., Ip N.Y., Peng H.B., Tsim K.W.K.;
A cysteine-rich form of Xenopus neuregulin induces the expression of acetylcholine receptors in cultured myotubes.";
                                                          Gaps
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093383; Q9W6NU;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Pro-neuregulin-1 precursor (Pro-NRG1) [Contains: Neuregulin-1]
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Length 695;
                                                       Indels
Score 2211; DB 2;
Pred. No. 2.5e-113;
                                                    Conservative 33; Mismatches
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Brain Res. Mol. Brain Res. 58:59-73(1998).
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66.1%;
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                          Similarity
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF076618; AAC26604.1; -.

R EMBL; AF142632; AAD33893.1; -.

R HSSP; Q12780; IHRE.

InterPro; IPR000742; EGF 2.

InterPro; IPR000509; EGF 1ike.

R InterPro; IPR00110; Ig-Tike.

R InterPro; IPR00110; Ig-Tike.

R Pfam; PF00008; EGF; 1.

R Pfam; PF00189; Neuregulin; 1.

R PRIMTS; PR01089; Neuregulin; 1.

R PRIMTS; PR01089; Neuregulin; 1.

R PROSITE; PS00022; EGF 1; 1.

R PROSITE; PS0026; EGF 3; 1.

R PROSITE; PS0038; IG-Tike; 1.
                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN: ERBB receptor binding is elicited entirely by the EGF-like
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Mol. Cell, Neurosci. 13:415-429(1999).

-I- FUNCTION: Direct ligand for the ERBB tyrosine kinase receptors.

Induces expression of acetylcholine receptor in synaptic nuclei.

-I- SUBCELLULAR LOCATION: Exists as a type I membrane protein and as a proteolytically released soluble growth factor form. The membrane-bound form does not seem to be active (By similarity).
                                                                                                                                                                                                               Name=CRD; Synonyms=CRD-NRG1, Cysteine-rich domain; lsoId=093183-2; Sequence=VSP 001449, VSP_001450 brain and TISSUE SPECIFICITY: Isoform alpha1 is expressed in brain and muscle. Isoform CRD is expressed in brain and spinal cord, but at
                                                                                                                                        Comment-Additional isoforms seem to exist. Isoforms have alphaor beta-type EGF-like domains;
                                                                                                                                                                                                                                                                                very low level in muscle.

DEVELOPMENTAL STAGE: Strong expression in developing brain and spinal cord of the embryo. Also expressed in the myotomal muscle. DOWAIN: The cytoplasmic domain may be involved in the regulation of trafficking and proteolytic processing. Regulation of the proteolytic processing intracellular domain
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Extracellular (Potential).

Internal signal sequence (Potential).

Cytoplasmic (Potential).

Ig-like C2-type.

EGF-like.

By similarity.

By similarity.

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Pro-neuregulin-1, membrane-bound form similarity).
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Comment=Additional isoforms seem to exist.
                                                                                                                                                                                               IsoId=093383-1; Sequence=Displayed;
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CHAIN
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         MAEKKKVKEGKGRKGKGKKDRKGKKAEGSDGGAASPKLKE
TYGSVQEGKLVLKCQAVSEQPSLKFRWFKGEKELGAKNK
PDSKPEHIX LRGKKSSELDISKASSADNGEYKCMVSNQLG
NDTVTVNVTIVVK -> MSEDTAEGLQNGCSEQSSDPPSAE
                                               LQNEESMPETQDEEETTHGITGLAITCCVCLEADRLRICLN
SEKICIIPILACLISLCLCIAGLKWVFVDKIFEYDSPTHLD
                                                                 PGHRGQDLLLYTDTAPSTLVPSSVRTLPVIIPTTDSKAAVT
FKFGTSLLPTE (in isoform CRD).
/FTId=VSP 003449.
                                                                                                PNEFTGD
                                                                                                                                                                                 1 MSER---KEGRG-KGKKKKERGSGKKPESAAGSQSPALPPQLKEMKSQESAAGSKLVLR
                                                                                                                                                                                             177 TKRG-----DITAGPGHLIKCSDKEKTYCVNGGECYVLNGITSSNQFMCKCKPGFTG
                                                                                                                                                                                                                                                                                                                                                                            KORKKLHDRLRQSLRSERNNMMNIANGPHHP-NPPP-ENVQLVNQYVSKNVISSEHIVER
                                                                                                                                                                                                                                                                                                                                                                                         ETETSFSTSHYTSTTHHSTTVTQTPSHSWSNGLSESMISEKSYSVIVTSSVENSRHTSPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGPRGRINGTGGPRECNSFLRHARETPDSYRDSPHSERYVSAMTTPARMSPVDFHTPSSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -GPRGRINGIGGPRDC-SYLRHARDIPDSYRDSPHSERYVSAMTTPARMSPVEFKTPISP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KSPPSEMSPPVSSMTVSMPSMAVSPFMEEERPLLLVTPPRLREKKFDHH-PQ-----QFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STEGANTSSSTSTSTTGTSHLVKCAEKEKTFCVNGGECFMVKDLSNPSRYLCKCPNEFTG
                                                                                                                                                                                                                                                                                                                                      219 DRCQN----YVMASFYKHLGIEFMEAEELYQKRVLTITGICIALLVVGIMCVV-AYCKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SFHHNPAHDSNSLPASPLRIVEDEEYETTQEYEPAQEPVKKLANSRRAKRIKPNGHIANR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEVDSNTSSQSSNSESETEDERVGEDTPFLGIQNPLAASLEATPAFRLADSRTNPAGRFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                ^
                                                                                                                                                                52;
                                                                                            KPGFTGARCTETDPLRVVRSEKHLGIEFWE
RCONYVMASFYK (in isoform CRD).
/FTId=VSP_003450.
                                                                                                                                            62.8%; Score 2102; DB 1; Length 677; 64.1%; Pred. No. 2.3e-107;
                                                                                                                                                               86; Mismatches 105; Indels
                                                                                                                          49279E8F5BAE396F CRC64;
                                                                                                                          75794 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOEELQARLSSVIANO 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||||:|||||||
TQEELQARLSS-IANQ 660
                                                                                                                                                              Conservative
 130
                                                                                                                          677 AA;
                                                                                                                                                     Best Local Similarity
Matches 433; Conserv
                                                                                              223
CARBOHYD
VARSPLIC
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462 AA.

Q7RTW1 PRELIMINARY; PRT; Q7RTW1; 01-MAR-2004 (TrEMBLrel. 26, Created)

RESULT 13 Q7RTW1

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                                                                                                                                                                                                                                                                                                                                                                   The feature of the fe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 DSASANITIVESNEIITGMPASTEGAYVSSESPIRISVSTEGANTSSSTSTSTTGTSHLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EELYQKRVLTITGICIALLVVGIMCVVAYCKTKKQRKKLHDRLRQSLRSERNNMNIANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHHPNPPPENVQLVNQYVSKNVISSEHIVEREAETSFSTSHYTSTAHHSTTVTQTPSHSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNGHTESILSESHSVIVMSSVENSRHSSPIGGPRGRLNGTGGPRECNSFLRHARETPDSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MSERKEGRGKGKGKKKRERGSGKKPESAAGSQSPALPPQLKEMKSQESAAGSKLVLRCETS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSERKEGRGKGKKKERGSGKKPESAAGSQSPALPPRLKEMKSQESAAGSKLVLRCETS
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                                                                                                                                                                             Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5;
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Pred. No. 2.2e-106;
3; Mismatches 16; Indels 5;
                                                                                                                                                                             Craniata, Vertebrata, Eutelo
Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF02158; Neuregulin; 1.
PRINTS; PR01089; NEUREGUIN.
PROSITE; P800022; EGF 1.
PROSITE; P801186; EGF 2; 1.
PROSITE; P850026; EGF 3; 1.
SEQUENCE 462 AA; 50848 MW; 8CAADBB30056A80D CRC64;
          Last sequence update)
Last annotation update)
                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62.2%;
01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, Neuregulin 1 isoform ndf43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 405; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00008; EGF; 1.
Pfam; PF00047; ig: 1.
                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                 PubMed=12145742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   н
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61 WFKNGNELNFKNKPQNIKIQKKPGKSELRINKASLADSGEYMCKVISKLGNDSASANITI 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 VESNEIITGMPASTEGAYVSSESPIRISVSTEGANTSSSTSTSTTGTSHLVKCAEKEKTF 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 190 CVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCQNYVMASFYKHLGIEFMEAEELYQKRVL 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KGKGKKKDRGSGKKPAPADGGPSPALPPRLKEMKSQESAAGSKLVLRCETSSEYSSLRFK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 KGKGKKKERGSGKKPESAAGSQSPALPPQLKEMKSQESAAGSKLVLRCETSSEYSSLRFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neuregulin 1 alpha isoform (Fragment).
Oyytochagus cuniculus (Rabbit).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | I] | BOUGHOUR FROM N.A. | BUDUCK J. | BOUGHOUR FROM N.A. | BUDDICK J. | SUDMITTED (SEP-2003) to the EMBL/GenBank/DDBJ databases. | SUDMITTED (SEP-2003) to the EMBL/GenBank/DDBJ databases. | SIMILAMITY: Contains 1 EGF-like domain. | BEMBL, AY421758; AAR00250.1; - | SIMILAMITY: Contains 1 EGF-like domain. | R GO; GO:0005100; F:receptor binding; IEA. | R GO; GO:0005100; F:receptor binding; IEA. | R GO; GO:000790; P:embryonic development; IEA. | R GO; GO:000790; P:embryonic development; IEA. | R InterPro; IPR006219; IEGF. | R InterPro; IPR006219; IGG. | R InterPro; IPR006219; IGG. | R InterPro; IPR005598; IGG. | R InterPro; IPR005598; IGG. | R InterPro; IPR005598; IGG. | R InterPro; IPR005159; R INTERPO; IPR005159; R INTERPRO; IPR005159; R INTERPRO; IPR005159; R INTERPRO; IPR005159; R INTERPRO; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         394 AA; 42980 MW; C183EE80927443F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                             05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 56.0%; Score 1875.5; DB Best Local Similarity 91.7%; Pred. No. 3.2e-95; Matches 366; Conservative 6; Mismatches 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWART; SW00408; IGC2; 1.
PROSITE; PS00022; EGF 1; 1.
PROSITE; PS01086; EGF 2; 1.
PROSITE; PS50026; EGF 3; 1.
PROSITE; PS50036; IG_IKE; 1.
EGF-11Ke domain.
NON_TER
NON_TER
SEQUENCE 394 AA, 42980 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS, PRO1089; NEUREGULIN.
SWART; SMO0181; EGF; 1.
SWART; SMO0409; IG; 1.
                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                   420 YRDSPHSERY 429
                                                                                                                                                                       NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                       Q6TGK9;
                                                                                                                                                                                                                                                                                                                           Q6TGK9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AEELYQKRVLTITGICIALLVVGIMCVVAYCKTKKQRKKLHDRLRQSLRSERNNMMNIAN 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GPHHPNPPPENVQLVNQYVSKNVISSEHIVEREAETSFSTSHYTSTAHHSTTVTQTPSHS 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             235 AEELYQKRVLTITGICIALLVVGIMCVVAYCKTKKQRQKLHDRLLGSLRSERNNWVNIAN 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Velasco J.A., Feijoo E., Avila M.A., Notario V.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
-- SIMILARITY: Contains 1 EGF-like domain.
EMBL; U96612; AAB71812.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                461 AA; 50890 MW; 935C9560F7148336 CRC64;
                                                                                                                                                                                                                                       01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0005102; F:receptor binding; IEA.
GO; GO:0005102; F:receptor binding; IEA.
InterPro: IPR000742; EGF 2.
InterPro: IPR006209; EGF 1.
InterPro: IPR006210; IEGF.
InterPro: IPR006210; IEGF.
InterPro: IPR00110; Ig-11ke.
InterPro: IPR00110; Ig-11ke.
InterPro: IPR00116; Ig-11ke.
InterPro: IPR00116; IGF; IG-11ke.
InterPro: IPR00116; IGF; IG-11ke.
InterPro: IPR00116; IGF; IG-11ke.
Pfam; PF00104; Ig; I.
Pfam; PF00104; Ig; I.
Pfam; PF00108; IGF; I.
PROSTTF; SM01089; IGC2; I.
PROSTTF; PS001186; EGF 1; I.
PROSTTF; PS0026; EGF 2; I.
PROSTTF; PS0035; IG_IKE; I.
EGF-11ke domain.
SEQUENCE 461 AA; 50890 MW; 935C9560F7148336
                                                                                                                                                                                           461 AA.
                                                                                                                                                                                                                                                                                                                                                 Mesocricetus auratus (Golden hamster).
                                                                                                                                                                                     PRELIMINARY;
RDSPHSERY 429
                                 ||||||||||
RDSPHSERH 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
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421
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| Qy | 250 TITGICIALLVVGIMCVVAYCKTKKQRKKLHDRLRQSLRSERNNMMNIANGPHHPNPPPE 309 | 236 TITGICIALLVVGIMCVVAYCKTKKQRKKLHDRLRQSLRSERNNMVNIANGPHHPNPPPE 295 | 236 TITGICIALLVVGIMCVVAYCKTKKQRKKLHDRLRQSLRSERNNMVNIANGPHHPNPPPE 295 | 237 NVQLVNQVVSKNVISSEHIVERAETSFSTSHYTSTAHHSTTVTQTPSHSWSNGHTESIL 369 | 296 NVQLVNQYVSKNVISSEHIVEREAETSFSTSHYTSTAHHSTTVTQTPSHSWSNGHTESIL 355 | Qy | 370 SESHSVIWMSSVENSRHSSPTGGPRGRLNGTGGPRECNS 408 | 256 SESHSVIWMSSVENSRHSSPTGGPRGRLNGTGGPRECNS 394 | 256 SESHSVIWMSSVENSRHSSPTGGPRGRLNGTGGGPRECNS 394 | 256 SESHSVIWMSSVENSRHSSPTGGPRGRLNGTGGPRECNS 394 | 256 SESHSVIWMSSVENSRHSPTGGPRGRLNGTGGPRECNS 394 | 256 SESHSVENSRHSPTGGPRGRLNGTGGPRECNS 394 | 256 SESHSVENSRHSPTGGPRGRLNGTGGPRECNS 394 | 256 SESHSVENSRHSPTGGPRGRLNGTGGPRECNS 394 | 256 SESHSVENSRHSPTGGPRGRLNGTGGPRECNS 394 | 256 SESHSVENSRHSPSPTGGPRGRLNGTGGPRGCNS 394 | 256 SESHSVENSRHSPSPTGGPRGRLNGTGGPRECNS 394 | 256 SESHSVENSRHSPSPTGGPRGRLNGTGGPRGCNS 394 | 256 SESHSVENSRHSPSPTGGPRGRLNGTGGP
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Search completed: April 12, 2005, 14:33:51 Job time : 187 secs

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us-10-082-747a-93.rpr

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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April 12, 2005, 14:26:42 ; Search time 48 Seconds (without alignments) 1292.913 Million cell updates/sec Run on:

1 MSERKEGRGKGKGKKKERGS.....QEEIQARLSSVIANQDPIAV 645 US-10-082-747A-93 3347 Title: Perfect score: Sequence:

283416 segs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

283416

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hereonlin, splice	ρ		neu differentiatio	neu differentiatio	neu differentiatio	acetylcholine rece	neu differentiatio	neu differentiatio	herequlin precurso	glial growth facto	neu differentiatio	ErbB kinase activa					heregulin isoform	neu differentiatio	sensory/motor neur	neuregulin-3 [impo		protein T6D22.14 [	hypothetical prote	nucleolus-cytoplas	neural cell adhesi	hypothetical prote	ᆽ	·
SUMMARIES		B43273	~	A43273	161718	161722	161719	A45769	I38404	I38403	D43273	832359	A56210	JC5701	JC5700	JC5702	S32357	I38408	S62676	I38405	A56943	T44447	PC4415	D86215	T34513	B42680	IJCHNL	T13594	T13893	
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		3343	3280	3202.5	3066.5	3058.5	2980	2526.5	2086.5	1751.5	1183	1098	1059	1028	993	992	827	788	545.5	485	351	334.5	182.5	181	179	172	171	170	169	
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probable serine/th protein UNC-89 - C	nypotnetical prote MSB2 protein - yea probable villin 2 Alaetic titin - hu	microtubule-associ neural cell adhesi anna arctein - vea	carbon catabolite hypothetical prote nucleolar phosphop	mycelial surface a hypothetical prote regulatory protein serine-rich protei
T18611 T29757	T16201 S25370 E84845 T38346	T13564 JN0635 874285	S70704 T24008 I38073	T17415 E86185 S61112 T39903
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30	3 8 8 4 4 4 4 4	36	) E 4 4 0 0 0 1	4 4 4 4 0 6 4 0

## ALIGNMENTS

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A;Accession: I38406
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule 'type: mRNA
A;Molecule 'type: mRNB', 'F', '420-645 <RES>
A;Cross-references: EMBL:U02328; NID:g408406; PIDN:AAA19953.1; PID:g408407
C;Genetics:
A;Genetics:
C;By2-8pli
A;Genetics:
A;Geneti
B43273
heregulin, splice form beta 1 - human
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Length 645;

ö 61 SEYSSLRFKWFKNGNELNRKNKPQNIKIQKKPGKSELRINKASLADSGEYMCKVISKLGN 120 61 SEYSSLRFKWFKNGNELNRKNKPQNIKIQKKPGKSELRINKASLADSGEYMCKVISKLGN 120 180 180 9 1 MSERKEGRGKGKKKKERGSGKKPESAAGSQSPALPPRLKEMKSQESAAGSKLVLRCETS 121 DSASANITIVESNEIITGMPASTEGAYVSSESPIRISVSTEGANTSSSTSTSTTGTSHLV 121 DSASANITIVESNEIITGMPASTEGAYVSSESPIRISVSTEGANTSSSTSTSTTGTSHLV 1 MSERKEGRGKGKKKKERGSGKKPESAAGSQSPALPPQLKEMKSQESAAGSKLVLRCETS Gaps ö Indels ö 99.9%; Score 3343; DB 2; 99.8%; Pred. No. 1.3e-183; iive 1; Mismatches 0; 644; Conservative Query Match Best Local Similarity Matches 644; Conserv g 셤 셤 ઠે ઠ ઠે ઠે

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N

180 240 232 300 292 360

352

420 412 480

472

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532

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Addationate names: breat cancer call differentiation factor p45; Neu differentiation facing bergulin precursor, splice form alpha - human NyAlerante names: breat cancer call differentiation factor p45; Neu differentiation (5)Species: Homo saptens (man)
C;Species: Homo saptens (man)
C;Species: Homo saptens (man)
C;Species: Homo saptens (man)
C;Species: Homo saptens (man)
S;Holmes, W. B.; Silwkowski, M.X.; Akita, R.W.; Henzel, W.J.; Lee, J.; Park, J.W.; Yansur, S;Holmes, W. B.; Silwkowski, M.X.; Akita, R.W.; Henzel, W.J.; Lee, J.; Park, J.W.; Yansur, S;Holmes, W. B.; Silwkowski, M.X.; Akita; R.W.; Henzel, W.J.; Lee, J.; Park, J.W.; Yansur, S;Holmes, mucher: addaton of heregulin, a specific activator of p185(erbB2).
A;Ttle: Identification of heregulin, a specific activator of p185(erbB2).
A;Status: mucleic acid sequence not shown; not compared with conceptual translation A;Molecule type: mRNA
A;Residues: 1-640 cHOL
A;Residues: 20-21, XX,23-1840; MJD:9336731; PMID:7689552
A;Molecule type: protein
A;Residues: 20-21, XX,23-1840; MJD:93208945; PMID:1348215
A;Residues: 10-22, 1992
A;Title: Isolation of the neu/HER-2 stimulatory ligand; a 44 kd glycoprotein that induce A;Reference number: A38155; MUD:92208945; PMID:1348215
A;Residues: XX,15-16, 1992
A;Resid
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RPLLLVTPPRLREKKFDHHPQQFSSFHHNPAHDSNSLPASPLRIVEDEEYETTQEYEPAQ
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                                                                                                 KCAEKEKTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCQNYVMASFYKHLG1EFMEA
                                                                                                                                                                                                                 EELYQKRVLTITGICIALLVVGIMCVVAYCKTKKQRKKIHDRLRQSLRSERNNMMIANG
                                                                                                                                                                                                                                                                                                                                            PHHPNPPPENVQLVNQYVSKNVISSEHIVEREAETSFSTSHYTSTAHHSTTVTQTPSHSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  353 SNGHTESILSESHSVIVMSSVENSRHSSPTGGPRGRLNGTGGPRECNSFLRHARETPDSY
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C;Superfamily: human heregulin; EGF homology; immunoglobulin homology
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A,Cross-references: GDB:132656; OMIM:142445
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Cipacies: Jubec-1993 #sequence_revision 31-Dec-1993 #text_change 08-Sep-2002
Cipacies: Jubec-1993 #sequence_revision 31-Dec-1993 #text_change 08-Sep-2002
Cipacies: Jubec-1993 #sequence_revision 31-Dec-1993 #text_change 08-Sep-2002
Cipacies: Jubec-1993 #sequence_revision of heregulin, a specific activator of pl85 (erbB2).
A;Title: Identification of heregulin, a specific activator of pl85 (erbB2).
A;Reference number: A43273
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual trans, molecule type: mRNA
A;Residues: 1-637 *HOLD
A;Residues: 1-637 *HOLD
A;Residues: 1-637 *HOLD
A;Reference number: A56210; MUID: 941S8863; PMID: 7509448
A;Title: Structural and functional aspects of the multiplicity of Neu differentiation fance and appearance of the multiplicity of Neu differentiation fance and control or all and functional expects of the multiplicity of Neu differentiation fance and appearance and functional expects of the multiplicity of Neu differentiation fance and appearance and functional expects of the multiplicity of Neu differentiation fance and appearance and functional experiments
A;Residues: 119-406 *RES>
A;Residues: 119-406 *RES>
A;Residues: 119-406 *RES>
A;Genetics:
A;G
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C43273
heregulin precursor, splice form beta-2 - human
C;Species: Homo sapiens (man)
C;Species: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 08-Sep-2002
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                                        241 EELYQKRVLTITGICIALLVVGIMCVVAYCKTKKORKKLHDRLROSLRSERNNMMNIANG
                                                                                                                                                            301 PHHPNPPPENVQLVNQXVSKNVISSEHIVEREAETSFSTSHYTSTAHHSTTVTQTPSHSW
                                                                                                                                                                                                                                                                                      361 SNGHTESILSESHSVIVMSSVENSRHSSPTGGPRGRLNGTGGPRECNSFLRHARETPDSY
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C;Superfamily: human heregulin; EGF homology; immunoglobulin homology
C;Keywords: alternative splicing
F;182-221/Domain: EGF homology <EGF>
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: 161722
R;Wen, D.; Suggs, S.V.; Karunagaran, D.; Liu, N.; Cupples, R.L.; Luo, Y.; Janssen, A.M., Mol. Cell. Biol. 14, 1909-1919; 1994
A;Title: Structural and functional aspects of the multiplicity of Neu differentiation f A;Reference number: A56210; MUID:94158863; PMID:7509448
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary;
A;Residues: 1-662 «RES»
A;Residues: 1-662 «RES»
A;Cross-references: UNIPROT:P43322; EMBL:U02322; NID:g408394; PIDN:AAA19947.1; PID:g4082
C;Superfamily: human heregulin; EGF homology; immunoglobulin homology
F;182-221/Domain: EGF homology «EGF»
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A,Residues: 1-298,386,70',388,TR',391 <RE3>
A;Cross-references: EMBL:U02320; NID:9408390; PIDN:AAA19945.1; PID:9408391
C;Superfamily: human heregulin; EGF homology; immunoglobulin homology
F;182-221/Domain: EGF homology <EGF>
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                                                                                                                                                        91.6%; Score 3066.5; DB 2; Length 636; 91.6%; Pred. No. 8e-168; ive 22; Mismatches 23; Indels 9;
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161722
neu differentiation factor - rat
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Matches 591; Conservative
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C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: 161718; 161720
R;Wen, D: Suggs, S.V.; Karunagaran, D.; Liu, N.; Cupples, R.L.; Luo, Y.; Janssen, A.M.;
Mol. Cell. Biol. 14, 1909-1919, 1994
A;Title: Structural and functional aspects of the multiplicity of Neu differentiation fa
A;Reference number: A56210; MUID:94158863; PMID:7509448
A;Reference number: A56210; MUID:94158863; PMID:7509448
A;Reference number: A56210; MUID:94158863; PMID:7509448
A;Residues: L636 RES>
A;Cossion: 161718
A;Residues: L-636 RES>
A;Cossion: 161721
A;Rattus: preliminary; translated from GB/EMBL/DDBJ
A;Rocession: 161721
A;Residues: L444, A', 446-636 RES>
A;Rossicues: EMBL:U02321; NID:9408392; PIDN:AAA19946.1; PID:9408393
A;Rocession: 161720
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                                                                     DB 2;
                                                                   Score 3202.5; DB 2;
Pred. No. 1.4e-175;
1; Mismatches 15;
  C;Keywords: alternative splicing; glycoprotein F;182-221/Domain: EGF homology <EGF>
                                                                   Query Match
Best Local Similarity 96.7%;
Matches 624; Conservative
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  Length 662
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                                         Indels
  DB 2;
                                         28;
  Score 3058.5; DB 2
Pred, No. 2.4e-167;
                                       25; Mismatches
91.4%;
89.1%;
                    Best Local Similarity 89.19
Matches 591; Conservative
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A; Residues: 1-422, "HK," NL', 637-638, 'ELRRNKAYRSKCMQIQLSATHLRPSSITHLGFIL' <RE3>
A; Cross-references: EMBL:U02316; NID:9408382; PIDN:AAA19941.1; PID:9408383
A; Accession: 16177
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-422, "H', 'NL', 637-638, 'ELRRNKAYRSKCMQIQLSATHLRPSSITHLGFIL' <RE4>
A; Cross-references: EMBL:U02317; NID:9408384; PIDN:AAA19942.1; PID:9408385
A; Accession: 161724
A; Cross-references: EMBL:U02317; NID:9408384; PIDN:AAA19942.1; PID:9408385
A; Accession: 161724
A; Molecule type: mRNA
A; Residues: 1-422 <RE5>
A; Residues: 1-42 <RE5>
A; Residues: L. 2 Cupples, R.; Suggs, S.V.; Bacus, S.S.; Luo, Y.; Trail, G.; Hu, S.; Call 69, 559-572, 1992
A; Title: Neu differentiation factor: a transmembrane glycoprotein containing an EGF dome A; Accession: A38220; MUID:92257596; PMID:1349853
A; Accession: A38220
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-422 <MEN>
A; Resi
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Cross-references: EMBL:U02323; NID:g408396; PIDN:AAA19948.1; PID:g408397
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89.0%; Score 2980; DB 2; 1
Best Local Similarity 89.6%; Pred. No. 7e-163;
Matches 579; Conservative 25; Mismatches 34;
                                      A;Accession: 161716
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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neu differentiation factor - human (5/species: Homo sapiens (man) (Homo sapiens) (Homo sa
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CiSpecies: Homo sapiens (man)

CiSpecies: Homo sapiens (man)

CiDate: 29-May-1998 #sequence_revision 29-May-1998 #text_change 08-Sep-2002

CiAccession: 138403

RiWen, D.; Suggs, S.V.; Karunagaran, D.; Liu, N.; Cupples, R.L.; Luo, Y.; Janssen, A.M., Mol. (Cell. Biol. 14, 1909-1919, 1994

A.Title: Structural and functional aspects of the multiplicity of Neu differentiation for A.Reference number: A56210; MUID:94158863; PMID:7509448

A.Accession: 138403

A.Molecule type: mRNA

A.Molecule type: mRNA

A.Molecule type: mRNA

A.Residues: 1-350 cRES

A.Residues: 1-350 cRES

A.Coros-references: EMBL:002325; NID:9408400; PIDN:AAA19950.1; PID:9408401

C.Superfamily: human heregulin; EGF homology; immunoglobulin homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 62.3%; Score 2086.5; DB 2; Length Best Local Similarity 94.6%; Pred. No. 5.2e-112; Matches 406; Conservative 3; Mismatches 15; Indels
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R; Falls, D.L.; Rosen, K.M.; Corfas, G.; Lane, W.S.; Fischbach, G.D.
C; Accession: 45769
R; Falls, D.L.; Rosen, K.M.; Corfas, G.; Lane, W.S.; Fischbach, G.D.
Call 72, 1993
A; Title: ARIA, a protein that stimulates acetylcholine receptor synthesis, is a member c A; Reference number: A45769; MUD: 93201602; PMID: 8453670
A; Accession: A45769
A; Accession: A5769
A; Residues: 1-602 < PML>
A; Residues: 1-602 < PML>
A; Residues: 1-602 < PML>
A; Cross-references: UNIPROT: Q05199; GB: L11264; NID: 9212603; PIDN: AA449037.1; PID: 9212604
A; Experimental source: brain
A; Note: sequence extracted from NUBI backbone (NCBIN: 127787, NCBIP: 127788)
C; Superfamily: human heregulin; EGF homology; immunoglobulin homology
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                                                                                                                                                                          C;Species: Gallus gallus (chicken)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MCVVAYCKTKKQRKKLHDRLRQSLRSERNNMMIANGPHHPNPPPENVQLVNQYVSKNVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SRHTSPT-GPRGRLNGIGGPREGNSFLRHARETPDSYRDSPHSERYVSAMTTPARMSPVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144 EGAYVSSESPIRISVSTEGANTSSSTSTSTTGTSHLVKCAEKEKTFCVNGGECFMVKDLS
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                                                                                                                                                    acetylcholine receptor synthesis stimulator ARIA-1 precursor - chicken
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LAASLEVAPAFRLAESRTNPAGRFSTQEELQARLSSVIANQDPIAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 75.5%; Score 2526.5; DB 2; Best Local Similarity 77.2%; Pred. No. 5.3e-137; Matches 480; Conservative 54; Mismatches 51;
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Cy 181 KCAEKEKTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONYVMASFY 230	
QY         194 GECFMVKDLSNPSRYLCKCPNEFTGDRCQNYVMASFYKHLGIEFMEAEELYQKRVLT         250           Db         1 GECFMVKDLSNPSRYLCKCQPGFTGARCTENVPMKYQNQEKHLGIEFLAEELYQKRVLT         60           QY         251 ITGICIALLVVGIMCVVAYCKTKKQRKKLHDRLQSLRSERNNMMYIANGPHHPNPPPEN         120           QY         311 VQLVNQYVSKRVISSEHIVEREAETSFSTSHYTSTAHHSTTVTQTPSHSWSNGHTESILS         370           Db         121 VQLVNQYVSKRVISSEHIVEREAETSFSTSHYTSTAHHSTTVTQTPSHSWSNGHTESILS         180           QY         371 ESHSVIVMSSVENSRHSSPTGGPRGRLNGTGGPRECNSFLRHARETPDSYRDSPHSERYY         430           Db         121 VQLVNQYVSKNVISSEHIVEREAETSFSTSHYTSTAHHSTTVTQTPSHSWSNGHTESILS         180           QY         371 ESHSVIVMSSVENSRHSSPTGGPRGRLNGTGGPRECNSFLRHARETPDSYRDSPHSERYY         240           QY         431 SAMTTPARMSPVDPHTPSSPKSPPSEMSPPVSSMTVSMPSMAVSPPMEEBRPLLLVTPPR         300           QY         431 SAMTTPARMSPVDFHTPSSPKSPPSEMSPPVSSMTVSMPSMAVSPPMEEBRPLLLVTPPR         300           QY         491 IRREKKPDHHPQQPSSFHHNPAHDSNSLPASPLRIVVBDEEYETTQEYEPAG         540           Db         301 LREKKFDHHPQQPSSFHHNPAHDSNSLPASPLRIVEDEEYETTQEYEPAG         540           Db         301 LREKKFDHHPQQPSSFHHNPAHDSNSLPASPLRIVEDEEYETTQEYEPAG         540	National Description of the part of the pa

Db 61 KNGNELNRKNKPENIKIQKKPGKSELRINKASLADSGEYMCKVISKLGNDSASANITIVE 120	
132 SNEIITGMPASTEGAYVSSESPIRISVSTEGANTSSSTSTSTTGTSHLVKCAEKEKTFCV	OY 515NSLPASPLRIVEDEEYETTOEYEPAQEPVKKIANSRRAKRTK 556
121	
QY         192 NGGECFMVKDLSNPSRYLCKCPNEFTGDRCQNYVMASFY         230           D         181 NGGECFTVKDLSNPSRYLCKCPNEFTGDRCQNYVMASFY         219	
RESULT 13	Qy 605 EATPAFRLADSRT 617
JCS701 ErbB kinase activator alphal, brain and thymus - rat	828 USFFUCFAAUSKI
C;Species: Rattus norvegicus (Norway rat) C;Date: 25-Nov-1997 #sequence_revision 25-Nov-1997 #text_change 09-Jul-2004	
R.H.Gashiyama, S.; Horikaw, M.; Yamada, K.; Ichino, N.; Nakano, N.; Nakagawa, T.; Miyag J. Biochem. 122, 675-680, 1997	
A;Title: A novel brain-derived member of the epidermal growth factor family that inter A;Reference number: JC5700; MUID:98006324; PMID:9348101 A;Acession: JC5701	ac C; Accession: JCS700 R; Higashiyama, S.; Horikawa, M.; Yamada, K.; Ichino, N.; Nakano, N.; Nakagawa, T. J. Biochem. 122, 675-680, 1997
A;Morecule Lype: Makk A;Residues: 1-868 <hig> A:Arcoss:for: PCA41:</hig>	60 P P;
A; McDecule type: protein A; McBecule type: protein A; Residues: 128-162 <h12></h12>	c
A;Experimental source: PC-12 cell C;Comment: This protein is a member of the epidermal growth factor family. It is functi ating the differentiation of MDA-MB-453 cells.	44.
C;Superfamily: human ErbB kinase activator alpha, brain and thymus; EGF homology; i F;361-397/Domain: EGF homology <egf></egf>	or alpha, brain and thymus; EGF homology;
Query Match 30.7%; Score 1028; DB 2; Length 868; Best Local Similarity 37.7%; Pred. No. 3.4e-51; Matches 254; Conservative 97; Mismatches 188; Indels 134; Gaps 21:	C:Keywords: glycoprotein F;258-311/Domain: Ig-like #status predicted <igl> F;345-381/Domain: EGF homology <egf> F:346-381/Domain: EGF-like #status predicted <egf></egf></egf></igl>
11 GKGKKKERGSGKKPESAAGSQSPALPPQLKEMKSQESAAGSKLVLRCETSSEYSSLRFKW 7	(Asn
Db 234 GKNIKKEVGKILCTDCATRPKLKKWKSQTGEVGEKQSLKCEAAAGNPQPSYFW 286	Query Match 29.7%; Score 993; DB 2; Length 850; Best Local Similarity 37.1%; Pred, No. 3.3e-49; Matches 250; Conservative 98: Mismatches 189: Indels 136: Gaps 22:
Qy 71 FKNGNELARKNKPQNIKIQKKPGKSELRINKASLADSGEYMCKVISKLGNDSASANIT 128	11 GKGKKKERGSGKKPESAAGSQSPALPPOLKEMKSQESAAGSKLVLRCETSSEYSSLRFKW 7
	218 GKNLKKEVGKILCTDCATRPKLKKMKSQTGQVGEKQSLKCEAAAGNPQPSYRW 27
Db 344 V	Oy 71 FKOGNELNEKNEPONIKIQKKPGKSELRINKASLADSGEYMCKVISKLGNDSASANIT 128 
QY 189 FCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCQNYVMASFYKHLGIEFMEAEE 242	129 IVESNEIITGMPASTEGAYVSSESPIRISVSTEGANTSSSTSTGTGTSHLVKCAEKEKT 18
QY         243 LYQKRVLTITGICIALLVVGIMCVVAXCKTKKQRKKLHDRLRQSLRSERNNMMIANGPH 302           Db         425 LYQKRVLTITGICVALLVVGIVCVVAXCKTKKQRRQMHHLIRQNMCPAHQN-RSLANGPS 483	DD 327
Qy 303 HPNPPPENVQLVNQYVSKAVISSEHIVEREAETSFSTSHYTSTAHHSTTVTQTPS 357	Db 352 YCVNGGVCYXIEGINQLSCKCPNGFEGRCLEKLPLRLYMPDFRQKAEELYQKRV 406 OV 249 LITIGICIALLVVGIMCVVAYCKTKKORKKIHDRIROSIRSERNNMMNIANGPHHPNPPP 308
Db 484 HPRLDPEELQMAD-YISKNVPATDHVIRREAETTFSGSHSCSPSHHCSTATPTSSHRHES 542  Ov 358 HEGENGHTBETI GEGHTINGGETENGEBER AGENT AGENTER AGENT	
	Qy 309 ENVQLVNQYVSKNVISSEHIVEREAETSFSTSHYTSTAHHSTTVTQTPSHSWSNG 363   : :  :  :       ::  ::
QY 417 PDSYRDSPHSERYVSAMTTPARMSPVDFHTPSSPKSPPSEMSPPVSSMTVSMPSM 471	364 HTESILSESHSVIVMSSVENSRHSSPT-GGPRGRLNGTGGPRECNSFLRHARETP 41
Qy 472 A-VSPPMEBERPLILVTPPRLREKKFDHHPQQFSSFHHNPAHDS 514 	DD 525 RSESLISDSQSGIMLSSVGTSKCNSPACVEARARRAAARNLEERRRAIAPPYHDSV 580 QY 418 DSYRDSPHSERYVSAMITPARMSPVDFHIPSSPKSPPSEMSPPVSSMIVSMPSMA-VSPF 476

OY 309 ENVQLVNQYVSRAVISSEHIVEREAETSFSTSHYTSTAHHSTTVTQTPSHSWSNG 363	704 GGSLGSLPASPFRIPEDDEYETTQECAPPPPRPRTRGASRRTSAGPRRWRRSRLNGLAA 563 NRLEVDSNTSSQSSNSESETEDERVGEDTPPLGIQNPL-AASLEATPAF 	Search completed: April 12, 2005, 14:42:49 Job time : 50 secs	
Db 581 DSLRDSPHSERYVSALTTPARLSPVDFHYSLATQVPTFEITSPNSAHAVSLPPAAPISYR 640  Qy 477 MEERPLLLYTPPRLREKKFDHHPQQFSSFHHNPAHDS 514	RESULT 15 UC5702 ExbB kinase activator alpha2a, brain and thymus - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 25-Nov-1997 #sequence_revision 25-Nov-1997 #text_change 09-Jul-2004 C;Accession: JC5702; PC4417 R;Higashiyama, S.; Horikawa, M.; Yamada, K.; Ichino, N.; Nakano, N.; Nakagawa, T.; Miyag J; Blochem. 122, 675-680, 1997 A;Title: A novel brain-derived member of the epidermal growth factor family that interact A;Reference number: JC5700; MUID:98006324; PMID:9348101	A; Status: nucleic, acid sequence not shown A; Molecule type: mRNA A; Molecule type: mRNA A; Residues: 1-860 < LHIS A; Cross-references: UNIPKOT:03556; DDBJ:DB9996; NID:g2605631; PIDN:BAA23345.1; PID:g260 A; Experimental source: PC-12 cell A; Accession: PC4417 A; Status: nucleic acid sequence not shown A; Molecule type: mRNA A; Residues: 'F', 212-213,223-860 < HIZ> A; Cross-references: DDBJ:AB001576; NID:g2605478; PIDN:BAA23348.1; PID:g2605479 A; Experimental source: PC-12 cell C; Comment: This protein is a member of the epidermal growth factor family. It is function the differentiation of MDA-MB-453 cells. C; Superimentally: human ErbB kinase activator alpha, brain and thymus; EGF homology; immunc C; Keyworfs: glycoprotein F; 274-327/Domain: Ig-11ke #status predicted < HGL>F; 261-327/Domain: Ig-11ke #status predicted < HGL>F; 224-44/Domain: hydrophobic #status predicted < HSD>F; 163, 294, 467/Binding site: carbohydrate (Asn) (covalent) #status predicted	Query Match         29.6%;         Score 992;         DB 2;         Length 860;           Best Local Similarity         37.2%;         Pred. No. 3.8e-49;         Indels 130;         Gaps 21;           Matches 248;         Conservative 99;         Mismatches 190;         Indels 130;         Gaps 21;           QY         11 GKGKKKERGSGKKPESAAGSQSPALPPQLKEMKSQESAAGSKLVLRCETSSEXSLRFKW 70